STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 151322

TO: Elizabeth McElwain
Location: REM-2A11/2C18
Art Unit: 1638
Thursday, April 28, 2005

Case Serial Number: 10/088079

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner McElwain,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

151522

STIC-Biotech/ChemLib

From: McElwain, Elizabeth
Sent: Friday, April 22, 2005 3:50 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Please search 10/088,079 - SEQ ID NO: 1 and 2, and DNA encoding SEQ ID NO: 2 for prior art and for interference.
Thank you,
Beth

Elizabeth F. McElwain, Ph.D.
U.S. Patent and Trademark Office
Tech Center 1600, Art Unit 1638
room Remsen 2A11
mailbox Remsen 2C18
571-272-0802
elizabeth.mcelwain@uspto.gov

4/27/05
1 - AA - Ø1
1 - PA - Ø2
remarks AA
4/28/05

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 10:53:47 ; Search time 40 Seconds
(without alignments)
815.437 Million cell updates/sec

Title: US-10-088-079-2
Perfect score: 1722
Sequence: 1 MNQRNASMTVIGAGSYGTAL.....AREAALTLLGRARKDERSSH 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1719	99.8	339	2	S47829	glycerol-3-phospha
2	1719	99.8	339	2	G86036	glycerol-3-phospha
3	1719	99.8	339	2	F91189	glycerol-3-phospha
4	1640	95.2	339	2	AB0975	glycerol-3-phospha
5	1455	84.5	339	2	AD0009	glycerol-3-phospha
6	1242	72.1	344	2	A82050	glycerol-3-phospha
7	1150	66.8	335	2	F64080	glycerol-3-phospha
8	751.5	43.6	346	2	H82637	glycerol-3-phospha
9	703	40.8	332	2	C97111	glycerol 3-phospha
10	672.5	39.1	338	2	AH1316	NAD(P)H-dependent
11	669.5	38.9	338	2	AH1688	NAD(P)H-dependent
12	666.5	38.7	345	2	H69636	glycerol-3-phospha
13	631	36.6	345	2	H83854	NAD(P)H-dependent
14	624.5	36.3	329	2	E81953	glycerol-3-phospha
15	621	36.1	336	2	T35643	glycerol-3-phospha
16	613.5	35.6	341	2	B86792	hypothetical prote
17	608.5	35.3	334	2	C70673	probable gpdA2 pro
18	607	35.2	327	2	AI2901	glycerol-3-phospha
19	607	35.2	327	2	C97677	probable glycerol-
20	605.5	35.2	338	2	C98109	glycerol-3-phospha
21	604.5	35.1	338	2	E95244	glycerol-3-phospha
22	601.5	34.9	326	2	AI3273	glycerol-3-phospha
23	599.5	34.8	332	2	B89926	glycerol-3-phospha
24	575.5	33.4	331	2	E87257	glycerol-3-phospha
25	567	32.9	349	2	T45431	glycerol-3-phospha
26	567	32.9	351	2	A87119	glycerol-3-phospha
27	556	32.3	340	2	H83443	glycerol-3-phospha
28	547	31.8	334	2	A81743	glycerol-3-phospha
29	546	31.7	334	2	G72024	glycerol-3-phospha
30	546	31.7	334	2	E86597	glycerol-3-P dehyd
31	532	30.9	334	2	A71480	probable glycerol-
32	515	29.9	341	2	C70932	probable dehydroge
33	505	29.3	328	2	H75251	glycerol-3-phospha
34	502.5	29.2	313	2	A70441	glycerol-3-phospha
35	482	28.0	330	2	S75139	glycerol-3-phospha
36	460	26.7	354	2	T48649	glycerol-3-phospha
37	448	26.0	307	2	AG2017	glycerol-3-phospha
38	422.5	24.5	433	2	F84832	glycerol-3-phospha
39	415	24.1	356	2	E71252	probable glycerol-
40	403	23.4	312	2	H71876	glycerol-3-phospha
41	403	23.4	312	2	A64640	glycerol-3-phospha
42	381	22.1	298	2	F81325	glycerol-3-phospha
43	366.5	21.3	316	2	A71703	glycerol-3-phospha
44	350	20.3	321	2	E69147	glycerol-3-phospha
45	350	20.3	325	2	G97776	hypothetical prote

ALIGNMENTS

RESULT 1
S47829
glycerol-3-phosphate dehydrogenase (NAD) (EC 1.1.1.8) - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47829; B65161
R;Plunkett, G.
submitted to the EMBL Data Library, March 1994
A;Reference number: S47666
A;Accession: S47829
A;Molecule type: DNA
A;Residues: 1-339 <PLU>
A;Cross-references: UNIPROT:P37606; EMBL:U00039; NID:g466582; PIDN:AAB18585.1; PID:g1657
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B65161
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-339 <BLAT>
A;Cross-references: GB:AE000439; GB:U00096; NID:g1790036; PIDN:AAC76632.1; PID:g1790037;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: gpsA
C;Superfamily: glycerol-3-phosphate dehydrogenase (NAD)
C;Keywords: oxidoreductase

Query Match 99.8%; Score 1719; DB 2; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.2e-118;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
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Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339


RESULT 2
G86036
glycerol-3-phosphate dehydrogenase (NAD+) [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G86036
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G86036
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <STO>
A;Cross-references: UNIPROT:P37606; GB:AE005174; NID:g12518358; PIDN:AAG58755.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: gpsA
C;Superfamily: glycerol-3-phosphate dehydrogenase (NAD)

  Query Match             99.8%;  Score 1719;  DB 2;  Length 339;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-118;
  Matches  338;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339


RESULT 3
F91189
glycerol-3-phosphate dehydrogenase (NAD+) [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C;Accession: F91189
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91189
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <HAY>
A;Cross-references: UNIPROT:P37606; GB:BA000007; PIDN:BAB37909.1; PID:g13363961; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4486
C;Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)

  Query Match             99.8%;  Score 1719;  DB 2;  Length 339;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-118;
  Matches  338;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
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Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339


RESULT 4
AB0975
glycerol-3-phosphate dehydrogenase (NAD) (EC 1.1.1.8) - Salmonella enterica subsp. enter
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004
C;Accession: AB0975
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0975
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03294.1; PID:g16504915; GSPDB:GN00176
C;Genetics:
A;Gene: gpsA
C;Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)
C;Keywords: oxidoreductase

  Query Match             95.2%;  Score 1640;  DB 2;  Length 339;
  Best Local Similarity   94.7%;  Pred. No. 7.3e-113;
  Matches  321;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||| |||||||||||||||||||||||||:|||||||:|||||| |||| |||||||||
Db          1 MNQSNASMTVIGAGSYGTALAITLARNGHQVVLWGHDPKHIATLEHDRCNVAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              |||||||||||||||||||||||||| :|||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFSDVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDETFADDLQQLLHCGKSFRVY 180
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Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              | |||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db        181 INADFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLTEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:|||||||||||||||||: ||:|||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVKGAQDKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||:| | |
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKEELSRH 339


RESULT 5
AD0009
glycerol-3-phosphate dehydrogenase (NAD) (EC 1.1.1.8) [imported] - Yersinia pestis (stra
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 16-Aug-2004
C;Accession: AD0009
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0009
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <KUR>
A;Cross-references: UNIPROT:Q8ZJM6; GB:AL590842; PIDN:CAC88934.1; PID:g15978181; GSPDB:G
C;Genetics:
A;Gene: gpsA
C;Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)
C;Keywords: oxidoreductase

  Query Match             84.5%;  Score 1455;  DB 2;  Length 339;
  Best Local Similarity   84.2%;  Pred. No. 2.7e-99;
  Matches  283;  Conservative   24;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||   ||| |||||||||||||||||:||||||||:||  |::|||| |||||  ||
Db          1 MNTNPASMAVIGAGSYGTALAITLARNGHQVVLWGHDPKHIQQLQQDRCNRAFLPDAAFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||| ||:||| |||||::|||||||||| || |:|| :| |||:||||||||||||||
Db         61 DTLRLETDLACALAASRDVLVVVPSHVFGAVLHQLKPHLRKDARIVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              |||||| ||: |||||||||||||||||||||||:|||||  |::|||||||||||||||
Db        121 QDVAREVLGEAIPLAVISGPTFAKELAAGLPTAIALASTDVQFSEDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
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Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMTRLGTALGADPSTF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:|||||||||:|||||: |: ||: |||||||||||||||  || |
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGIMLGQGLGVKEAQDNIGQVVEGYRNTKEVLALAQRH 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDER 336
              ||||||||:||||||| |||||||||||||| :|||:
Db        301 GVEMPITEQIYQVLYCHKNAREAALTLLGRTKKDEK 336


RESULT 6
A82050
glycerol-3-phosphate dehydrogenase (NAD+) VC2651 [imported] - Vibrio cholerae (strain N1
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 16-Aug-2004
C;Accession: A82050
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82050
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <HEI>
A;Cross-references: UNIPROT:Q9KNT0; GB:AE004331; GB:AE003852; NID:g9657236; PIDN:AAF9579
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2651
A;Map position: 1
C;Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)

  Query Match             72.1%;  Score 1242;  DB 2;  Length 344;
  Best Local Similarity   74.5%;  Pred. No. 1.1e-83;
  Matches  245;  Conservative   32;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          8 MTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPDTLHLES 67
              |||||||||||:|||:|||||  :|||||| ||:| |: || |  ||| : ||||| :|:
Db         16 MTVIGAGSYGTSLAISLARNGANIVLWGHDAEHMARLDADRANHEFLPGIAFPDTLIVET 75

Qy         68 DLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLLQDVAREA 127
              ||  |: |||::|||||||||| ||: ::| :| |:|: ||||||| |||||||||  :
Db         76 DLQKAVQASRDLLVVVPSHVFGIVLKSLQPHLRADSRICWATKGLEPETGRLLQDVAHDV 135

Qy        128 LGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVYSNPDFIG 187
              |||  ||||:|||||||||| |:|||||:|| |  |  |||: :|| |:||||:| ||||
Db        136 LGDSYPLAVLSGPTFAKELAMGMPTAISVASPDAQFVRDLQEKIHCSKTFRVYANSDFIG 195

Qy        188 VQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATFMGMAGLG 247
              :|||||||||||||||||||||||||||||||||||||||||||||||| | |||||||||
Db        196 MQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGAQPETFMGMAGLG 255

Qy        248 DLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEMPIT 307
              |||||||:|||||||||: |||| || :||  ||||||||||||||  || | ||||||
Db        256 DLVLTCTDNQSRNRRFGLALGQGKDVDTAQTDIGQVVEGYRNTKEVWMLAKRMGVEMPIV 315

Qy        308 EEIYQVLYCGKNAREAALTLLGRARKDER 336
              |:|||||| ||:|| ||  || | :| ||
Db        316 EQIYQVLYQGKDARLAAQDLLARDKKMER 344


RESULT 7
F64080
glycerol-3-phosphate dehydrogenase (NAD) (EC 1.1.1.8) - Haemophilus influenzae (strain R
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004
C;Accession: F64080
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: F64080
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-335 <TIGR>
A;Cross-references: UNIPROT:P43798; GB:U32743; GB:L42023; NID:g1573597; PIDN:AAC22264.1;
C;Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)
C;Keywords: oxidoreductase

  Query Match             66.8%;  Score 1150;  DB 2;  Length 335;
  Best Local Similarity   67.4%;  Pred. No. 6e-77;
  Matches  221;  Conservative   48;  Mismatches   59;  Indels    0;  Gaps    0;

Qy          8 MTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPDTLHLES 67
              :||:|||||||||||| :|||    ||||:| ||| :: :| |  ||||| ||: |||||
Db          8 ITVLGAGSYGTALAITFSRNGSPTHLWGHNPAHIAQMQTERQNYRFLPDVIFPEDLHLES 67

Qy         68 DLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLLQDVAREA 127
```

```
              :|| |:  |::||:||||| |||:| :||| ::   ||:|||||||  ||||||  |  |
Db         68 NLAQAMEYSQDILIVVPSHAFGEILIKIKPHLKAHHRLIWATKGLERNTGRLLQTVVEEQ 127

Qy        128 LGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVYSNPDFIG 187
              || | ||||:|||||||||| |||:||:||: :: || : |  :|| | |||| | |  |
Db        128 LGTQYPLAVLSGPTFAKELAQGLPSAITLAANNEQFAREFQSRIHCSKGFRVYINSDMTG 187

Qy        188 VQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATFMGMAGLG 247
              ||||||:|||||||||:|||:||||||||||||||:||::||| :|||:  |||||:|||
Db        188 VQLGGAIKNVIAIGAGISDGMGFGANARTALITRGIAEITRLGISLGANTNTFMGMSGLG 247

Qy        248 DLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEMPIT 307
              |||||||:|||||||||:|||:|:| | | | |||||||: ||||   || | |||||||
Db        248 DLVLTCTDNQSRNRRFGLMLGKGLDAQMAMENIGQVVEGFYNTKEAYLLAQRQGVEMPIT 307

Qy        308 EEIYQVLYCGKNAREAALTLLGRARKDE 335
              |:|||:|:|||:|:: |::||||| | |
Db        308 EQIYQMLFCGKSAQDVAISLLGRACKGE 335


RESULT 8
H82637
glycerol-3-phosphate dehydrogenase XF1802 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82637
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H82637
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <SIM>
A;Cross-references: UNIPROT:Q9PCH7; GB:AE004001; GB:AE003849; NID:g9106864; PIDN:AAF8461
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1802
C;Superfamily: glycerol-3-phosphate dehydrogenase (NAD)

  Query Match             43.6%;  Score 751.5;  DB 2;  Length 346;
  Best Local Similarity   46.7%;  Pred. No. 1e-47;
  Matches  156;  Conservative   54;  Mismatches  111;  Indels   13;  Gaps    3;

Qy          8 MTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPDTLHLES 67
              : |:||||:|||||  :||: :  :||| |   | :::  | |  :|| :  | ||   :
Db          8 IAVLGAGSWGTALAALVARHAYPTILWGRDVGVIQSIDIQRQNFRYLPSIMLPQTLRATT 67

Qy         68 DLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLLQDVAREA 127
              ||| |:: :  :|| |||: | | ||:: ||:     : ||||| |  :|| | :||||
Db         68 DLAAAVSGADWVLVAVPSYAFTETLRRLAPLLSTGVGVAWATKGFEPGSGRFLHEVAREI 127

Qy        128 LGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVYSNPDFIG 187
              ||   ||||::||:||||:  |||||:::      |   :  :| |  || |:  | ||
Db        128 LGGDAPLAVVTGPSFAKEVTLGLPTAVTVHGEYARFTQMVANAMH-GPMFRAYTGNDVIG 186

Qy        188 VQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATFMGMAGLG 247
              :||||:|||:|:  |::||:  | |||  ||||| || || | :|| | | ||:||||
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```
Db        187 AELGGAMKNVLAVAIGVADGMQLGMNARAGLITRGLNEMLRLSAVIGARPETLMGLAGLG 246

Qy        248 DLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEMPIT 307
              ||||||| : ||||| |  ||:|  :  |  :||||||  : : ||   | : |||:||:
Db        247 DLVLTCTGDLSRNRRLGFALGRGQSLSDAIREIGQVVESVQTSDEVMRQAEQHGVELPIS 306

Qy        308 EEIYQVL------YCGKNAREAALTLLGRARKDE 335
              | :  ||      | |  |      || | :| |
Db        307 EAVRAVLREEITPYAGMKA------LLAREQKPE 334


RESULT 9
C97111
glycerol 3-phosphate dehydrogenase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 16-Aug-2004
C;Accession: C97111
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97111
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332 <KUR>
A;Cross-references: UNIPROT:Q97ID6; GB:AE001437; PIDN:AAK79678.1; PID:g15024677; GSPDB:GN
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1712
C;Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)

  Query Match             40.8%;  Score 703;  DB 2;  Length 332;
  Best Local Similarity   42.1%;  Pred. No. 3.5e-44;
  Matches  138;  Conservative   71;  Mismatches  117;  Indels    2;  Gaps    2;

Qy          8 MTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPDTLHLES 67
              :| || ||:|||||| ||: || ||:|  : | :  :   | |  :||:    | :
Db          4 VTFIGGGSFGTALAIMLAKKGHNVVIWDRNKEILEDINTLRTNTRYLPNNIIPCCVKAVD 63

Qy         68 DLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLLQDVAREA 127
              |:  |   |: |:: |||    || |:||  :| |  ::   ||:| || : | :| :|
Db         64 DIEKAAKESKYIVLAVPSFAIREVCRKIKGFLREDQIIISIAKGMEEETKKRLSEVVKEE 123

Qy        128 LGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVYSNPDFIG 187
              |    |: |:|||: |:|:|  :|| : : |||  :|:::| :     |||||:| | :|
Db        124 LYKN-PVVVLSGPSHAEEVANDIPTTVVVTSTDMKYAEEVQDVF-MTNSFRVYTNSDIVG 181

Qy        188 VQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATFMGMAGLG 247
              |::||||||:||: :|: ||||:| | : ||:|||::|: |:|  ||  | || |: |:|
Db        182 VEIGGAVKNIIALASGIGDGIGYGDNTKAALMTRGMSEIMRIGVKLGGKPETFFGLTGMG 241

Qy        248 DLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEMPIT 307
              ||::|||   ||||: |:::|:||  : | :|||  |||| :      ||    || ||||
Db        242 DLIVTCTSMHSRNRKAGILIGRGMSCREACDKIGMVVEGVKACHTFYELKESLGVSMPIT 301

Qy        308 EEIYQVLYCGKNAREAALTLLGRARKDE 335
              :|:||:   : ::    |: | :|:|
Db        302 TSLYKVLFENGDPKKEVYELMARDKKNE 329


RESULT 10
AH1316
NAD(P)H-dependent glycerol-3-phosphate dehydrogenase homolog gpsA [imported] - Listeria
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C;Accession: AH1316
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
```

```
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1316
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-338 <GLA>
A;Cross-references: UNIPROT:Q8Y5W9; GB:NC_003210; PIDN:CAD00014.1; PID:g16411389; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: gpsA
C;Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)

  Query Match             39.1%;  Score 672.5;  DB 2;  Length 338;
  Best Local Similarity   39.4%;  Pred. No. 6.1e-42;
  Matches  134;  Conservative   79;  Mismatches  122;  Indels    5;  Gaps    3;

Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
                | |:    : ::|||:|| ||: || | |: |:||:  : :  :      |: :|||:  |
Db          1 MTQK--KVAILGAGSWGTGLALVLADNNHKPVIWGNLDKIVNEINESHTNSHYLPDIILP 58

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
                 :       |  |:  :  ::: :|::      | :|:    ::     ||  :||:| ||    :
Db         59 TEVKATLSLDEAIDGAEIVVIAIPTNAMRIVCKQLNEALKEPTILVHVSKGIEPETNLRM 118

Qy        121 QDVAREAL--GDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFR 178
               :|  |  :    :   | |:|||: |:|:|    || :   :   | : |: :|         : |
Db        119 SEVIEEEIDAAKRKALVVLSGPSHAEEVALRHPTTLCASCKDLSAAEIVQDRF-INNNLR 177

Qy        179 VYSNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPA 238
               :|:| | || ::|||:||:||:|||:|||:| || ||:|||:||::||| |:|::|
Db        178 IYTNDDVIGAEIGGALKNIIALGAGISDGLGYGDNAKAALMTRGMAEITRLGVAVGSNPQ 237

Qy        239 TFMGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAH 298
               || |: |:|||::|||    |||  |  | |||:|  ::       ||:| |||| |   | |    |
Db        238 TFYGLTGIGDLIVTCTSVHSRNWRAGNMLGKGENLDEVLEKMGMVVEGVRTAKAVHGWAK 297

Qy        299 RFGVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSS 338
               :  ::||||| || :|:   |:||||     |:|| :| |: |
Db        298 KLDIDMPITESIYAILFENKDAREAVDLLMGREKKIEKES 337
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RESULT 11

```
AH1688
NAD(P)H-dependent glycerol-3-phosphate dehydrogenase homolog gpsA [imported] - Listeria
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C;Accession: AH1688
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1688
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-338 <GLA>
A;Cross-references: UNIPROT:Q92A72; GB:AL592022; PIDN:CAC97280.1; PID:g16414551; GSPDB:G
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: gpsA
C;Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)

  Query Match             38.9%;  Score 669.5;  DB 2;  Length 338;
  Best Local Similarity   39.4%;  Pred. No. 1e-41;
  Matches  134;  Conservative   78;  Mismatches  123;  Indels    5;  Gaps    3;

Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
                | |:    : ::|||:|| ||: || | |: |:||:  : :  :      |: :|||:  |
Db          1 MTQK--KVAILGAGSWGTGLALVLADNNHKPVIWGNLDKIVNEINESHTNSHYLPDIILP 58

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
                 :      |  |:  :  ::: :|::      | :|:    ::     ||  :||:| ||    :
Db         59 TEVKATLSLDEAIDGAEIVVIAIPTNAMRVVCKQLNEALKEPTILVHVSKGIEPETNLRM 118

Qy        121 QDVAREALG--DQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFR 178
               :|  |  :    :   | |:|||: |:|:|    || :   :   | :  |: :|         : |
Db        119 SEVIEEEVDATKRKALVVLSGPSHAEEVALRHPTTLCASCKDLKAAEIVQDRF-INNNLR 177

Qy        179 VYSNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPA 238
               :|:| | || ::|||:||:||:|||:|||:| || ||:|||:||::||| |:|::|
Db        178 IYTNDDVIGAEIGGALKNIIALGAGISDGLGYGDNAKAALMTRGMAEITRLGVAVGSNPQ 237

Qy        239 TFMGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAH 298
               || |: |:|||::|||    |||  |  | |||:|  ::       ||:| |||| |   | |    |
Db        238 TFYGLTGIGDLIVTCTSVHSRNWRAGNMLGKGENLDEVLEKMGMVVEGVRTAKAVHGWAK 297

Qy        299 RFGVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSS 338
               :  ::||||| || :|:   |:||||     |:|| :| |: |
Db        298 KLDIDMPITESIYAILFENKDAREAVDLLMGRKKKIEKES 337
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RESULT 12

```
H69636
glycerol-3-phosphate dehydrogenase (NAD) (EC 1.1.1.8) gpsA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69636
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69636
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-345 <KUN>
A;Cross-references: UNIPROT:P46919; GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14199.
A;Experimental source: strain 168
C;Genetics:
A;Gene: gpsA
C;Superfamily: glycerol-3-phosphate dehydrogenase (NAD)
C;Keywords: oxidoreductase

  Query Match             38.7%;  Score 666.5;  DB 2;  Length 345;
  Best Local Similarity   40.3%;  Pred. No. 1.7e-41;
  Matches  133;  Conservative   78;  Mismatches  116;  Indels    3;  Gaps    2;

Qy          8 MTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPDTLHLES 67
               :|::||||:|||||:  |   ||:|| :|  |    :  |   :       |  :||:|     ::   :
Db          4 VTMLGAGSWGTALALVLTDNGNEVCVWAHRADLIHQINELHENKDYLPNVKLSTSIKGTT 63

Qy         68 DLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLLQDVAREA 127
               |:  |:: :  :| || ||:     ||||  |   :    |   :  :||:|  ::  : ::
Db         64 DMKEAVSDADVIIVAVPTKAIREVLRQAVPFITKKAVFVHVSKGIEPDSLLRISEIMEIE 123

Qy        128 LGDQI--PLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVYSNPDF 185
               |    :    : |:|||: |:|:       || :: :|      |:::| |        :||||:|||
Db        124 LPSDVRKDIVVLSGPSHAEEVGLRHPTTVTASSKSMRAAEEVQDLF-INHNFRVYTNPDI 182

Qy        186 IGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATFMGMAG 245
               |||::|||:||:||: ||::||:|:| ||: |||||||||::|||    :| :| || |: |
Db        183 IGVEIGGALKNIIALAAGITDGLGYGDNAKAALITRGLAEIARLGTKMGGNPLTFSGLTG 242
```

```
Qy        246 LGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEMP 305
              :|||::|||   |||  | | :||:|  ::   |::| |||| | ||   :|: :: |:||
Db        243 VGDLIVTCTSVHSRNWRAGNLLGKGYKLEDVLEEMGMVVEGVRTTKAAYQLSKKYDVKMP 302

Qy        306 ITEEIYQVLYCGKNAREAALTLLGRARKDE 335
              ||| ::|||: |:    |  :|: | :  |
Db        303 ITEALHQVLFNGQKVETAVESLMARGKTHE 332


RESULT 13
H83854
NAD(P)H-dependent glycerol-3-phosphate dehydrogenase gpsA [imported] - Bacillus halodura
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H83854
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H83854
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <STO>
A;Cross-references: UNIPROT:Q9KCD2; GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB053
A;Experimental source: strain C-125
C;Genetics:
A;Gene: gpsA
C;Superfamily: glycerol-3-phosphate dehydrogenase (NAD)

  Query Match             36.6%;  Score 631;  DB 2;  Length 345;
  Best Local Similarity   38.8%;  Pred. No. 6.9e-39;
  Matches  130;  Conservative   70;  Mismatches  123;  Indels   12;  Gaps    4;

Qy          7 SMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPD----T 62
              :: ||||||:||||:: || ||| | |      |    :      |  :|| :  |     |
Db          3 NVAVIGAGSWGTALSLVLADNGHHVTLVARREEIAREINERHTNETYLPSIEIPSSIVAT 62

Qy         63 LHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLLQD 122
                :|  :    :     |::|||:    : :| :  :::    :| |:||:|  :   : :
Db         63 CSMEEIIDVEI-----IVLVVPTKAIRQAVRSLNDVLKWPVTIVHASKGIEPGSHLRISE 117

Qy        123 VAREALGDQI--PLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              :  | |   :   : |:|||: |:|::   || ::::|   :    :| |    : ||||
Db        118 MIEEELEPTLLKEVVVLSGPSHAEEVSLRQPTTVTVSSKSLSTTKQIQDLF-MNQQFRVY 176

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              :| | |||::|||:||:||:  |:::|:|:| | : |::|||||: |||  ||| | ||
Db        177 TNEDLIGVEIGGALKNIIALACGLTNGLGYGDNTKAAIMTRGLAEIGRLGVKLGASPLTF 236

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
               |::|||||::|||   ||| | | |||:|     :| :| |||| | |:   ||| :
Db        237 AGLSGLGDLIVTCTSIHSRNWRAGQMLGKGKSPAEVEESMGMVVEGIRTTQAAHELAQKL 296

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDE 335
              :|||||  :| ||: ||    ||  |:|| :| |
Db        297 QIEMPITSALYSVLFEGKKPEHAADELMGRVKKHE 331


RESULT 14
E81953
glycerol-3-phosphate dehydrogenase (NAD) (EC 1.1.1.8) NMA0375 [imported] - Neisseria men
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Aug-2004
C;Accession: E81953
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81953
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-329 <PAR>
A;Cross-references: UNIPROT:Q9JWH0; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB8367
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: gpsA; NMA0375
C;Superfamily: Glycerol-3-phosphate dehydrogenase (NAD)
C;Keywords: oxidoreductase

  Query Match             36.3%;  Score 624.5;  DB 2;  Length 329;
  Best Local Similarity   42.0%;  Pred. No. 1.9e-38;
  Matches  140;  Conservative   68;  Mismatches  114;  Indels   11;  Gaps    4;

Qy          8 MTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPDTLHLES 67
              :|||||||:|||||:  :::|: | ||  : : :  ::  | |   ||   ||:|| : :
Db          3 ITVIGAGSWGTALALHFSQHGNRVSLWTRNADQVRQMQEARENKRGLPGFSFPETLEVCA 62

Qy         68 DLATALAASRNILVVVPSHVFG-----EVLRQIKPLMRPDARLVWATKGLEAETGRLLQD 122
              ||| ||  |  :|:|  : | |     |:|:|       |   :: | || | :|| |
Db         63 DLADALKDSGLVLIV--TSVAGLRSSAELLKQYGAGHLP---VLAACKGFEQDTGLLTFQ 117

Qy        123 VAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVYSN 182
              | :| | |   : |:|||:||:|||  || |: ||| :| : ::|   |:     |:| :
Db        118 VLKEVLPDNKKIGVLSGPSFAQELAKQLPCAVVLASENQEWVEELVPQLNT-SVMRLYGS 176

Qy        183 PDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATFMG 242
              | ||| :|||||||:||  |:|||: :| ||| ||:||||||::|| :|:|| | | ||
Db        177 TDVIGVAVGGAVKNVMAIATGLSDGLEYGLNARAALVTRGLAEITRLASAMGAQPKTMMG 236

Qy        243 MAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGV 302
              :||:|||:||||   ||||| |: | :| ::     :|| | ||    :||   | :: :
Db        237 LAGIGDLILTCTGALSRNRRVGLGLAEGKELHQVLVEIGHVSEGVSTIEEVFNTACKYQI 296

Qy        303 EMPITEEIYQVLYCGKNAREAALTLLGRARKDE 335
              :||||: : |::      ::    |: |: : |
Db        297 DMPITQTLLQLIRKEMTPQQVVERLMERSARFE 329


RESULT 15
T35643
glycerol-3-phosphate dehydrogenase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35643
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z21585
A;Accession: T35643
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-336 <MUR>
A;Cross-references: UNIPROT:Q9ZBS0; EMBL:AL034447; PIDN:CAA22402.1; GSPDB:GN00070; SCOEDB
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC7A1.03
C;Superfamily: glycerol-3-phosphate dehydrogenase (NAD)

  Query Match             36.1%;  Score 621;  DB 2;  Length 336;
  Best Local Similarity   41.9%;  Pred. No. 3.6e-38;
  Matches  139;  Conservative   49;  Mismatches  134;  Indels   10;  Gaps    3;

Qy         10 VIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPDTLHLESDL 69
              | | ||:|||     ||  | || |||         :   | |  :|| |  |: |    :|
Db          9 VFGTGSWGTAFGTVLADAGCEVTLWGRRAALADAVNSTRTNPDYLPGVELPENLRATTDA 68

Qy         70 ATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLLQDVAREALG 129
              | |    :   :: |||       |     ||: |   ||    ||:|  :   : :|     :|
Db         69 AEAARDADFTVLAVPSQTLRAGLADWTPLLAPGTVLVSLMKGVELGSAMRMSEV----IG 124

Qy        130 DQIP-----LAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVYSNPD 184
              |         :||::||  |:|:|| :| |  :|  |:| |  ||   |    || |:| |
Db        125 DVAKVGAERIAVVTGPNLAREIAARMPAAAVVACPDETVAQRLQAACHT-PYFRPYTNTD 183

Qy        185 FIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATFMGMA 244
```

```
                :| :||||||||| :  |::||:| | ||: :|||||||| :||| |||||| || |:|
Db        184 VVGCELGGAVKNVIGLAVGIADGMGLGDNAKGSLITRGLAETTRLGVALGADPLTFSGLA 243

Qy        245 GLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEM 304
              |||||| ||:   |||  ||  ||:|| ::       |  || :: : | :|| | ||:|
Db        244 GLGDLVATCSSPLSRNHTFGTNLGKGMTLEETNAVTKQTAEGVKSCESVLDLARRHGVDM 303

Qy        305 PITEEIYQVLYCGKNAREAALTLLGRARKDER 336
              |||| :  ::: ||:   |   |: |: | ||
Db        304 PITETVVAIVHEGKSPVVAVKELMSRSAKPER 335


Search completed: April 27, 2005, 11:03:28
Job time : 41 secs
```

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2005, 13:52:02 ; Search time 652 Seconds
(without alignments)
3077.902 Million cell updates/sec

Title: US-10-088-079-2
Perfect score: 1722
Sequence: 1 MNQRNASMTVIGAGSYGTAL.....AREAALTLLGRARKDERSSH 339

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10088079/runat_27042005_101459_11238/app_query.fasta_1.519
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10088079_@CGN_1_1_644_@runat_27042005_101459_11238 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1722	100.0	1020	5	AAF57428	Aaf57428 E. coli g
2	1719	99.8	1020	4	AAS52655	Aas52655 E. coli D
3	1719	99.8	1020	8	ACA32689	Aca32689 Prokaryot
4	1719	99.8	1020	13	ADT48853	Adt48853 Bacterial
5	1640	95.2	1020	8	ACA51335	Aca51335 Prokaryot
6	1635	94.9	1017	8	ACA31966	Aca31966 Prokaryot
7	1587	92.2	1017	8	ACA35838	Aca35838 Prokaryot
8	1587	92.2	1038	11	ACH97774	Ach97774 Klebsiell
9	1556	90.4	1023	8	ACA49224	Aca49224 Prokaryot
10	1455	84.5	1020	8	ACA54019	Aca54019 Prokaryot
11	1420	82.5	1023	10	ADF03046	Adf03046 Bacterial
12	1411	81.9	1011	8	ACA44463	Aca44463 Prokaryot
13	1393.5	80.9	1023	10	ACF70491	Acf70491 Photorhab
14	1393.5	80.9	69727	10	ACF65374	Acf65374 Photorhab
15	1393.5	80.9	110000	10	ACF67367_35	Continuation (36 o
16	1373	79.7	990	13	ADS45613	Ads45613 Bacterial
17	1372	79.7	990	13	ADT46572	Adt46572 Bacterial
18	1242	72.1	1035	8	ACA53490	Aca53490 Prokaryot
19	1192	69.2	1014	8	ACA43241	Aca43241 Prokaryot
20	1154	67.0	135356	13	ADT05646	Adt05646 Haemophil
21	1150	66.8	1008	4	AAS53331	Aas53331 Haemophil
22	1150	66.8	1008	8	ACA34182	Aca34182 Prokaryot
23	1150	66.8	110000	2	AAT42063_06	Continuation (7 of
c 24	1141	66.3	4711	13	ADT05428	Adt05428 Haemophil
c 25	864	50.2	781	6	ABQ21987	Abq21987 Oligonucl
26	864	50.2	781	6	ABQ21986	Abq21986 Oligonucl
27	827	48.0	781	6	ABQ21989	Abq21989 Oligonucl
c 28	827	48.0	781	6	ABQ21988	Abq21988 Oligonucl
29	806	46.8	987	8	ACA37060	Aca37060 Prokaryot
30	794.5	46.1	1002	13	ADT41591	Adt41591 Bacterial
31	794.5	46.1	1002	13	ADS63997	Ads63997 Bacterial
32	794.5	46.1	1020	13	ADS63622	Ads63622 Bacterial
33	751.5	43.6	1041	13	ADT42864	Adt42864 Bacterial
34	738.5	42.9	1002	13	ADS57169	Ads57169 Bacterial
35	720.5	41.8	1002	13	ADT41768	Adt41768 Bacterial
36	709.5	41.2	1020	8	ACA21995	Aca21995 Prokaryot
37	703	40.8	999	8	ACA27525	Aca27525 Prokaryot
38	694	40.3	1029	8	ACA29483	Aca29483 Prokaryot
39	692	40.2	1065	8	ACA33900	Aca33900 Prokaryot
40	692	40.2	1071	10	ADC90723	Adc90723 E. faeciu
41	681	39.5	1062	10	ADC91772	Adc91772 E. faeciu
42	677.5	39.3	1032	9	ADB08817	Adb08817 Alloiococ
43	677.5	39.3	1032	9	ADB08815	Adb08815 Alloiococ
44	677.5	39.3	1032	9	ADB08819	Adb08819 Alloiococ
45	677.5	39.3	110000	9	ADB12064_07	Continuation (8 of

ALIGNMENTS

RESULT 1
AAF57428
ID AAF57428 standard; DNA; 1020 BP.
XX
AC AAF57428;
XX
DT 11-JUN-2001 (first entry)
XX
DE E. coli gpsA2FR encoding DNA.
XX
KW Glycerol-3-phosphate dehydrogenase; G3PD; feedback inhibition; oil seed;
KW genetic transformation; fatty acid; glycerolipid; osmotic stress; gpsA;
KW gpsA2FR; allele; ds.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
FT CDS 1. .1020
FT /*tag= a
FT /product= "gpsA2FR"
FT mutation 765
FT /*tag= b
FT /note= "there is a point mutation at this position as
FT compared to the wild-type gpsA gene, which makes the gene
FT feed-defective; wild-type GAC codon is changed to GAA
FT codon"
XX
PN WO200121820-A1.
XX

PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-CA001096.
XX
PR 22-SEP-1999; 99US-0155133P.
XX
PA (CANA) NAT RES COUNCIL CANADA.
XX
PI Zou J, Wei Y, Periappuram C, Selvaraj G, Datla R;
XX
DR WPI; 2001-257996/26.
DR P-PSDB; AAB62189.
XX
PT Manipulating glycerol-3-phosphate metabolism of plant for enhancing
PT stress tolerance, altering fatty acid content in glycerolipids, by
PT expressing in plant feedback defective glycerol-3-phosphate dehydrogenase
PT gene.
XX
PS Claim 5; Fig 1; 39pp; English.
XX
CC The invention provides a method for genetically transforming a plant so
CC that it expresses a a heterologous glycerol-3-phosphate dehydrogenase
CC (G3PD) that is less sensitive to feedback inhibition than wild-type G3PD.
CC The method involves providing a vector comprising a DNA sequence encoding
CC G3PD that is less sensitive to feedback inhibition than wild-type G3PD
CC and transforming the plant with the vector. The method is useful for
CC expressing a heterologous G3PD less sensitive to feedback inhibition than
CC wild-type G3PD in an oil seed bearing plant, such as Arabidopsis thaliana
CC or Brassica. The vectors are useful for producing a genetically altered
CC plant having altered fatty acid content in its glycerolipids, especially
CC elevated levels of C16 fatty acids and increased osmotic stress tolerance
CC relative to the wild type. The present sequence represents the DNA
CC encoding the E. coli gpsA2FR protein. The gene gpsA2FR is an allele of
CC the E. coli gpsA gene, and encodes an altered version of the GPDH protein
CC defective in feedback inhibition. This gpsA2FR gene can be used in the
CC vectors and method of the invention
XX
SQ Sequence 1020 BP; 214 A; 274 C; 304 G; 228 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.46e-158	Length:	1020
Score:	1722.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-10-088-079-2 (1-339) x AAF57428 (1-1020)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCAC 1017
```

RESULT 2
AAS52655
ID AAS52655 standard; DNA; 1020 BP.
XX
AC AAS52655;
XX
DT 13-FEB-2002 (first entry)
XX
DE E. coli DNA for cellular proliferation protein #377.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
KW antibacterial; drug design.
XX
OS Escherichia coli.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX

PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU34796.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Claim 27; SEQ ID NO 6292; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence encodes an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.78e-158	Length:	1020
Score:	1719.00	Matches:	338
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.71%	Mismatches:	0
Query Match:	99.83%	Indels:	0
DB:	4	Gaps:	0

US-10-088-079-2 (1-339) x AAS52655 (1-1020)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGACAACCAGTCGCGTAAC 780

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCAC 1017
```

RESULT 3
ACA32689
ID ACA32689 standard; DNA; 1020 BP.
XX
AC ACA32689;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #14346.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Escherichia coli.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU28819.

```
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 20559; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.78e-158      Length:          1020
Score:                    1719.00        Matches:         338
Percent Similarity:       100.00%        Conservative:    1
Best Local Similarity:    99.71%         Mismatches:      0
Query Match:              99.83%         Indels:          0
DB:                       8              Gaps:            0

US-10-088-079-2 (1-339) x ACA32689 (1-1020)

Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||
Db        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGACAACCAGTCGCGTAAC 780

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCAC 1017

RESULT 4
ADT48853
ID   ADT48853 standard; cDNA; 1020 BP.
XX
AC   ADT48853;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Bacterial polynucleotide #23604.
XX
KW   Recombinant DNA construct; transformed plant; improved plant property;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW   pathogen tolerance; pest tolerance; plant disease resistance;
KW   cell cycle pathway modification; plant growth regulator;
KW   homologous recombination; seed oil yield; protein yield; carbohydrate;
KW   nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW   bacterial polynucleotide; gene; ss.
XX
OS   Bacteria.
XX
PN   US2003233675-A1.
XX
PD   18-DEC-2003.
XX
PF   20-FEB-2003; 2003US-00369493.
XX
PR   21-FEB-2002; 2002US-0360039P.
```

XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 47291; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.78e-158	Length:	1020
Score:	1719.00	Matches:	338
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.71%	Mismatches:	0
Query Match:	99.83%	Indels:	0
DB:	13	Gaps:	0

US-10-088-079-2 (1-339) x ADT48853 (1-1020)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGACAACCAGTCGCGTAAC 780

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCAC 1017
```

RESULT 5
ACA51335
ID ACA51335 standard; DNA; 1020 BP.
XX
AC ACA51335;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #32992.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Salmomella typhi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU47465.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 39205; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1020 BP; 217 A; 271 C; 316 G; 216 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.41e-150	Length:	1020
Score:	1640.00	Matches:	321
Percent Similarity:	97.05%	Conservative:	8
Best Local Similarity:	94.69%	Mismatches:	10
Query Match:	95.24%	Indels:	0
DB:	8	Gaps:	0

US-10-088-079-2 (1-339) x ACA51335 (1-1020)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACCAAAGTAATGCGTCAATGACAGTCATCGGTGCCGGCTCGTACGGCACCGCTCTC 60

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||:::||||||||||||||||||||||||||:::|||
Db         61 GCCATCACTCTGGCGAGAAACGGCCACCAGGTTGTCCTGTGGGGCCACGACCCAAAACAT 120

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              |||||||||||||   ||||||||||   ||||||||||||||||||||||||||||||
Db        121 ATCGCGACCCTGGAGCACGATCGCTGCAACGTCGCGTTCCTTCCCGATGTGCCTTTTCCC 180

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATACGTTACACCTGGAAAGCGACTTAGCAACCGCGCTGGCGGCCAGTCGTAACATTCTG 240

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              |||||||||||||||||||||||||   :::||||||||||||||||||||||||||||
Db        241 GTGGTGGTGCCAAGCCATGTTTTCAGCGACGTGCTGCGGCAGATTAAACCGCTGATGCGT 300

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGATGCGCGTCTGGTATGGGCGACCAAAGGCCTGGAAGCGGAAACGGGGCGCCTGTTG 360

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGATGTCGCTCGCGAGGCGTTAGGCGATCAAATCCCGCTGGCGGTGATTTCCGGTCCG 420

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGTTCGCTAAAGAGCTGGCGGCGGGTTTGCCGACGGCAATCTCGCTAGCCTCAACCGAT 480

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGACCTTTGCCGACGATCTCCAGCAACTGTTGCACTGCGGAAAAAGTTTTCGCGTCTAT 540

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCAATGCGGATTTTATCGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTGATTGCGATT 600

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCGCGGGGATGTCTGACGGCATCGGCTTCGGCGCGAACGCCCGCACGGCGCTAATCACG 660

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTGGACTGACCGAAATGTCGCGGCTTGGCGCAGCGCTTGGTGCCGATCCCGCCACCTTT 720

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        721 ATGGGGATGGCGGGTTTAGGCGATCTGGTGCTGACCTGTACCGACAACCAGTCGCGCAAC 780

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||||||||||||||:::   |||||:::||||||
Db        781 CGTCGTTTTGGCATGATGCTTGGCCAGGGCATGGACGTTAAAGGCGCGCAGGATAAGATT 840

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCCAGGTGGTCGAAGGCTATCGCAATACGAAAGAAGTTCGTGAATTGGCGCACCGTTTT 900

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTGTATTGCGGAAAAAACGCG 960

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
              ||||||||||||||||||||||||||||||||||:::|||   |||   |||
Db        961 CGCGAGGCAGCATTAACGTTATTAGGTCGCGCCCGCAAGGAAGAGCTGAGTCGCCAC 1017
```

RESULT 6
ACA31966
ID ACA31966 standard; DNA; 1017 BP.
XX
AC ACA31966;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #13623.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Enterobacter cloacae.
XX
PN WO200277183-A2.
XX

PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU28096.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 19836; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1017 BP; 207 A; 289 C; 312 G; 209 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.04e-149	Length:	1017
Score:	1635.00	Matches:	319
Percent Similarity:	97.35%	Conservative:	11
Best Local Similarity:	94.10%	Mismatches:	9
Query Match:	94.95%	Indels:	0
DB:	8	Gaps:	0

US-10-088-079-2 (1-339) x ACA31966 (1-1017)

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Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              |||:::      ||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGCACTGTTAATGCGTCAATGACTGTGATCGGTGCCGGCTCATACGGCACCGCTCTT 60

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db         61 GCCATCACGCTGGCAAGAAATGGTCACGAAGTGGTTCTCTGGGGCCACGACCCAAAACAT 120

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              ||||||||||||:::||||||||||||||||    ||||||||||||||||||||||||||
Db        121 ATCGCAACGCTGCAACGCGACCGTTGTAACGTGGCGTTTCTTCCGGACGTTCCGTTCCCC 180

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACTCCCTGCACCTTGAAAGCGACCTTGCGACCGCGCTGGCGGCCAGCCGCAACATTCTG 240

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              :::|||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        241 ATTGTGGTTCCGAGCCATGTATTTGGCGACGTGCTCCGTCAGATTAAGCCGCTGATGCGC 300

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGATGCGCGCATTGTCTGGGCGACAAAAGGACTGGAAGCCGAAACCGGACGCCTGCTG 360

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        361 CAGGACGTTGCCCGCGAAGCGCTGGGTGATGCGATCCCGCTGGCGGTCATCTCCGGCCCG 420

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTTTGCCAAAGAGCTGGCCGCTGGCCTGCCGACGGCGATTTCGCTGGCCTCCACCGAT 480

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
              |||   |||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGGCCTTCTCCGACGATCTTCAACAGCTGCTGCACTGCGGCAAGAGCTTCCGCGTCTAC 540

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAACCCCGATTTTATCGGCGTGCAACTGGGCGGTGCGGTGAAGAACGTGATTGCGATT 600

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCGCCGGGATGTCAGACGGCATTGGTTTTGGTGCCAATGCGCGTACGGCGCTGATCACC 660

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||    ||||||||||||||||||    ||||||||||||||||||||||||||
Db        661 CGAGGGCTAACCGAAATGTCCCGCCTGGGCGAAGCGCTGGGTGCCGATCCGGCCACCTTT 720

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        721 ATGGGAATGGCTGGCCTGGGCGACCTGGTGCTGACCTGTACCGATAACCAGTCTCGTAAC 780

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||||    ||||||:::    ||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGACAGGGCAGCGATGTTAAAGGCGCGCAGGAGAAGATT 840

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAGGTGGTTGAAGGCTACCGCAATACCAAAGAAGTCCGCGAGTTGGCGCACCGTTTC 900

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTGTCGAAATGCCAATAACCGAGGAAATTTATCAGGTATTGTATTGCGGAAAAAATGCG 960

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        961 CGCGAGGCAGCATTGACCTTATTAGGTCGTGCGCGCAAGGACGAGCGCAGCAGTAAC 1017
```

RESULT 7
ACA35838
ID ACA35838 standard; DNA; 1017 BP.
XX
AC ACA35838;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #17495.
XX

KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Klebsiella pneumoniae.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU31968.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 23708; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1017 BP; 194 A; 306 C; 319 G; 198 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.98e-145	Length:	1017
Score:	1587.00	Matches:	313
Percent Similarity:	95.58%	Conservative:	11
Best Local Similarity:	92.33%	Mismatches:	15
Query Match:	92.16%	Indels:	0
DB:	8	Gaps:	0

US-10-088-079-2 (1-339) x ACA35838 (1-1017)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||      ||||||:::|||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACGCACTTAATGCTGCAATGACTGTGATCGGTGCCGGCTCTTACGGCACCGCTCTT 60

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||||   |||||||||||||||||||||||:::|||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACCACGTTGTGCTGTGGGGCCATGACCCGAAACAT 120

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              ||||||||||||:::  ||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGCGACGCTGCAACACGATCGCTGCAACGCCGCGTTCCTTCCCGATGTGCCTTTCCCG 180

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        181 GATACGCTGCATCTTGAGAGCGACCTGGCCACCGCGCTGGCCGCCAGCCGCGACATCCTT 240

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        241 GTCGTGGTGCCGAGCCATGTATTCGGTCAGGTGTTACGCCAGATTAAACCGCTGATGCGT 300

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCGACGCGCGGCTGGTGTGGGCCACCAAAGGCCTTGAGGCCGAAACCGGCCGTCTGCTG 360

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        361 CAGGACGTGGCGCGTGAAGCGCTGGGCGATGATATTCCGCTGGCGGTGATCTCGGGGCCA 420

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        421 ACCTTCGCCAAAGAGCTGGCCGCCGGCCTGCCGACGGCGATTTCGCTGGCGGCCACGGAT 480

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
                    ||||||:::|||||||||:::|||||||||||||||||||||||||||||||||
Db        481 CCGCAGTTTGCGGAGGACCTTCAGCGCCTACTGCACTGCGGCAAAAGCTTCCGCGTCTAC 540

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCAACCCGGACTTTATCGGCGTGCAGCTCGGCGGCGCGGTGAAAAACGTCATTGCCATC 600

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGGGCAGGTATGTCGGACGGCATCGGCTTCGGCGCCAATGCGCGTACGGCGCTGATTACC 660

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||  ||||||||||||||||||||||||||||||||||  ||||||
Db        661 CGTGGGCTGGTGGAAATGTCCCGCCTCGGCGCGGCGCTGGGCGCCGATCCGGAAACCTTT 720

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        721 ATGGGCATGGCCGGCCTCGGTGACCTGGTGCTCACCTGCACCGACAACCAGTCCCGTAAC 780

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        781 CGTCGCTTCGGCATGATGCTCGGCCAGGGTATGGACGTGCAGAGCGCCCAGGACAAGATT 840

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||  |||
Db        841 GGCCAGGTGGTTGAAGGCTACCGCAATACCAAGGAAGTTCGCGTTCTGGCACAGCGTTTA 900

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        901 GGTGTCGAAATGCCAATAACCGAGGAAATTTATCAGGTATTGTATTGCGGAAAAATTGCG 960

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        961 CGCGAGGCAGCATTGACCTTATTGGGTCGCGCCCGCAAGGACGAGCGCAGCAGCAAT 1017
```

RESULT 8
ACH97774
ID ACH97774 standard; DNA; 1038 BP.

XX
AC ACH97774;
XX
DT 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polynucleotide seqid 3569.
XX
KW Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.
XX
OS Klebsiella pneumoniae.
XX
PN US6610836-B1.
XX
PD 26-AUG-2003.
XX
PF 27-JAN-2000; 2000US-00489039.
XX
PR 29-JAN-1999; 99US-0117747P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL, Osborne M;
XX
DR WPI; 2003-895346/82.
DR P-PSDB; ABO64223.
XX
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 3569; 932pp; English.
XX
CC The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This sequence encodes a Klebsiella
CC pneumoniae polypeptide of the invention
XX
SQ Sequence 1038 BP; 201 A; 310 C; 324 G; 203 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.12e-145	Length:	1038
Score:	1587.00	Matches:	313
Percent Similarity:	95.58%	Conservative:	11
Best Local Similarity:	92.33%	Mismatches:	15
Query Match:	92.16%	Indels:	0
DB:	11	Gaps:	0

US-10-088-079-2 (1-339) x ACH97774 (1-1038)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||      ||||||:::||||||||||||||||||||||||||||||||||||||
Db         19 ATGAACGCACTTAATGCTGCAATGACTGTGATCGGTGCCGGCTCTTACGGCACCGCTCTT 78

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||   ||||||||||||||||||||||:::|||
Db         79 GCCATCACCCTGGCAAGAAATGGCCACCACGTTGTGCTGTGGGGCCATGACCCGAAACAT 138

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              ||||||||||:::   ||||||||||||||||||||||||||||||||||||||||||
Db        139 ATCGCGACGCTGCAACACGATCGCTGCAACGCCGCGTTCCTTCCCGATGTGCCTTTCCCG 198

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        199 GATACGCTGCATCTTGAGAGCGACCTGGCCACCGCGCTGGCCGCCAGCCGCGACATCCTT 258

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        259 GTCGTGGTGCCGAGCCATGTATTCGGTCAGGTGTTACGCCAGATTAAACCGCTGATGCGT 318

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 TCCGACGCGCGGCTGGTGTGGGCCACCAAAGGCCTTGAGGCCGAAACCGGCCGTCTGCTG 378

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 CAGGACGTGGCGCGTGAAGCGCTGGGCGATGATATTCCGCTGGCGGTGATCTCGGGGCCA 438

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        439 ACCTTCGCCAAAGAGCTGGCCGCCGGCCTGCCGACGGCGATTTCGCTGGCGGCCACGGAT 498

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
              ||||||:::|||||||||:::||||||||||||||||||||||||||||||||||||
Db        499 CCGCAGTTTGCGGAGGACCTTCAGCGCCTACTGCACTGCGGCAAAAGCTTCCGCGTCTAC 558

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ATCAACCCGGACTTTATCGGCGTGCAGCTCGGCGGCGCGGTGAAAAACGTCATTGCCATC 618

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 GGGGCAGGTATGTCGGATGGCATCGGCTTCGGCGCCAATGCGCGTACGGCGCTGATTACC 678

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              |||||||||   ||||||||||||||||||||||||||||||||   ||||||
Db        679 CGTGGGCTGGTGGAAATGTCCCGCCTCGGCGCGGCGCTGGGCGCCGATCCGGAAACCTTT 738

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        739 ATGGGCATGGCCGGCCTCGGTGACCTGGTGCTCACCTGCACCGACAACCAGTCCCGTAAC 798

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        799 CGTCGCTTCGGCATGATGCTCGGCCAGGGTATGGACGTGCAGAGCGCCCAGGACAAGATT 858

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||   ||||||   |||
Db        859 GGCCAGGTGGTTGAAGGCTACCGCAATACCAAGGAAGTTCGCGTTCTGGCACAGCGTTTA 918

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        919 GGTGTCGAAATGCCAATAACCGAGGAAATTTATCAGGTATTGTATTGCGGAAAAATTGCG 978

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        979 CGCGAGGCAGCATTGACCTTATTGGGTCGCGCCCGCAAGGACGAGCGCAGCAGCAAT 1035
```

RESULT 9
ACA49224
ID ACA49224 standard; DNA; 1023 BP.
XX
AC ACA49224;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #30881.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Salmonella paratyphi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.

XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU45354.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 37094; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1023 BP; 219 A; 272 C; 313 G; 219 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.28e-142	Length:	1023
Score:	1556.00	Matches:	318
Percent Similarity:	96.17%	Conservative:	8
Best Local Similarity:	93.81%	Mismatches:	13
Query Match:	90.36%	Indels:	3
DB:	8	Gaps:	0

US-10-088-079-2 (1-339) x ACA49224 (1-1023)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              |||||||||   |||||||||||||||||||||||||||||||||||||||||||||   |||
Db          1 ATGAACCAAAGTAATGCGTCAATGACAGTCATCGGTGCCGGCTCGTACGGCACCCT-CTC 59

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              |||||||||||||||||||||||||:::|||||||||||||||||||||||||:::|||
Db         60 GCCATCACTCTGGCGAGAAACGGCCACCAGGTTGTCCTGTGGGGCCACGACCCAAAACAT 119

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              ||||||||||||||   ||||||||||   |||||||||||||||||||||||||||||
Db        120 ATCGCGACCCTGGAGCACGATCGCTGCAACGTCGCGTTCCTTCCCGATGTGCCTTTTCCC 179

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        180 GATACGTTACACCTGGAAAGCGACTTAGCAACCGCGCTGGCGGCCAGTCGTAACATTCTG 239

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              |||||||||||||||||||||||||   :::|||||||||||||||||||||||||||||
Db        240 GTGGTGGTGCCAAGCCATGTTTTCAGCGACGTGCTGCGGCAGATTAAACCGCTGATGCGT 299

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CCGGATGCGCGTCTGGTATGGGCGACCAAAGGCCTGGAAGCGGAAACGGGGCGCCTGTTG 359

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CAGGATGTCGCTCGCGAAGCGTTAGGCGATCAAATCCCGCTGGCGGTGATTTCTGGCCCG 419

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        420 ACGTTCGCTAAAGAATTGGCGGCGGGTTTGCG-ACGGCAATCTCTCTGGCCTCAACCGAT 478

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 GAGACCTTTGCCGACGATCTCCAGCAACTGTTGCACTGCGGAAAAAGTTTTCGCGTCTAT 538

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 ATCAATGCGGATTTTATCGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTGATTGCGATT 598

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 GGCGCGGGGATGTCTGACGGCATCGGCTTCGGCGCGAACGCCCGCACGGCGCTAATCACG 658

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        659 CGTGGACTGACCGAAATGTCGCGGCTTGGCGCACG-CTTGGCGCCGATCCCGCCACCTTT 717

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        718 ATGGGGATGGCGGGTTTAGGCGATCTGGTGCTGACCTGTACCGACAACCAGTCGCGCAAC 777

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||||||||||||:::   ||||||:::||||||
Db        778 CGTCGTTTTGGCATGATGCTTGGCCAGGGCATGGACGTTAAAGGCGCGCAGGATAAGATT 837

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 GGCCAGGTGGTCGAAGGCTATCGCAATACGAAAGAAGTTCGTGAATTGGCGCACCGTTTT 897

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 GGTGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTTTTGTATTGCGGAAAAAACGCG 957

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSerHis 339
              |||||||||||||||||||||||||||||||||||||:::|||   |||   |||
Db        958 CGCGAGGCAGCATTAACGTTATTAGGTCGCGCCCGCAAGGAAGAGCTGAGTCGCCAC 1014
```

RESULT 10
ACA54019
ID ACA54019 standard; DNA; 1020 BP.
XX
AC ACA54019;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #35676.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Yersinia pestis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX

PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU50149.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 41889; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1020 BP; 238 A; 238 C; 288 G; 256 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.69e-132	Length:	1020
Score:	1455.00	Matches:	283
Percent Similarity:	91.37%	Conservative:	24
Best Local Similarity:	84.23%	Mismatches:	29
Query Match:	84.49%	Indels:	0
DB:	8	Gaps:	0

US-10-088-079-2 (1-339) x ACA54019 (1-1020)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||         |||||||||  ||||||||||||||||||||||||||||||||||||
Db          1 ATGAACACCAACCCTGCTTCAATGGCTGTTATCGGTGCCGGATCTTACGGCACCGCATTA 60

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||:::|||
Db         61 GCTATCACACTGGCGCGTAATGGCCATCAAGTCGTGTTATGGGGCCATGACCCTAAACAT 120

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              |||       |||::::::||||||||||||   ||||||||||||||       ||||||
Db        121 ATTCAACAGCTGCAACAAGACCGCTGTAACCGCGCTTTCCTACCTGATGCTGCTTTCCCC 180

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              ||||||||   ||||||:::||||||||   ||||||||||||||||||:::::|||
Db        181 GATACGTTGCGATTGGAAACCGACTTAGCATGTGCGTTGGCTGCCAGCCGCGATGTGTTG 240

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||||   ||||||  |||:::||||||   :::|||
Db        241 GTCGTCGTGCCCAGCCATGTCTTTGGTGCTGTTTTACATCAGTTGAAGCCTCATCTACGT 300

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              |||||||||:::|||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGATGCACGTATCGTCTGGGCAACCAAAGGGCTAGAAGCTGAAACCGGCCGTCTGCTA 360

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||   ||||||:::  ||||||||||||||||||||||||||||
Db        361 CAGGATGTGGCCCGCGAAGTCTTGGGCGAGGCTATCCCGCTTGCCGTGATTTCTGGTCCA 420

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        421 ACGTTTGCCAAAGAATTGGCCGCGGGTTTGCCTACGGCGATTGCGTTGGCATCGACCGAT 480

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
              |||::::::||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGCAATTTAGCGAAGATCTGCAACAGTTATTGCACTGTGGAAAAAGCTTTCGAGTTTAC 540

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTAATCCTGATTTTATCGGGGTACAGCTTGGTGGCGCAGTGAAAAACGTGATTGCCATC 600

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGCAGGTATGTCCGATGGCATCGGTTTTGGTGCGAATGCCCGTACCGCTCTAATAACC 660

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||||||||||||:::||||||||   ||||||||||||||||||:::||||||
Db        661 CGCGGGTTAGCGGAGATGACGCGCTTAGGGACGGCATTAGGTGCCGATCCTTCCACCTTT 720

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        721 ATGGGCATGGCAGGGTTAGGCGATTTGGTGCTAACCTGCACAGATAACCAATCCCGTAAC 780

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||:::|||||||||||||||:::  |||:::  ||||||:::  |||
Db        781 CGCCGATTTGGCATTATGCTGGGTCAGGGGTTGGGGGTGAAGGAGGCGCAGGACAACATT 840

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAAGTGGTAGAAGGTTACCGTAATACCAAGGAAGTTCTGGCATTAGCACAGCGTCAT 900

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||||||||:::|||||||||||||||||||  |||||||||
Db        901 GGCGTCGAAATGCCAATAACTGAACAAATTTATCAAGTGTTGTATTGTCATAAGAATGCT 960

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGluArg 336
              |||||||||||||||||||||||||||||  :::||||||||||:::
Db        961 CGTGAGGCGGCTCTGACGTTGTTGGGGCGGACCAAAAAAGATGAAAAA 1008
```

RESULT 11
ADF03046
ID ADF03046 standard; DNA; 1023 BP.
XX
AC ADF03046;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bacterial polynucleotide #3331.
XX
KW Proteus mirabilis infection; bacterial infection; antibacterial;
KW immunostimulant; gene; ds.

```
XX
OS   Proteus mirabilis.
XX
PN   US6605709-B1.
XX
PD   12-AUG-2003.
XX
PF   05-APR-2000; 2000US-00543681.
XX
PR   09-APR-1999;   99US-0128706P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Breton GL;
XX
DR   WPI; 2003-895291/82.
DR   P-PSDB; ADF07218.
XX
PT   New Proteus mirabilis polypeptides and polynucleotides, useful as
PT   reagents for diagnosis of bacterial disease, as components of
PT   antibacterial vaccines, as targets for antibacterial drugs, or as
PT   biocontrol agents for plants.
XX
PS   Disclosure; SEQ ID NO 3331; 870pp; English.
XX
CC   The invention relates to new Proteus mirabilis polypeptides and
CC   polynucleotides. The invention also relates to antibodies against the
CC   polypeptides, methods for producing the polypeptides, a method of
CC   generating vaccines for immunising an individual against P. mirabilis, a
CC   method for evaluating a compound for the ability to bind a P. mirabilis
CC   polypeptide and a method for screening test compounds for anti-bacterial
CC   activity. The polypeptides and polynucleotides are useful as molecular
CC   targets for diagnosing, preventing and treating pathological conditions
CC   resulting from bacterial infection, as reagents for diagnosis of
CC   bacterial diseases, as components of antibacterial vaccines, as targets
CC   for antibacterial drugs or as bio-control agents for plants. This
CC   sequence represents a Proteus mirabilis polynucleotide of the invention.
XX
SQ   Sequence 1023 BP; 266 A; 206 C; 264 G; 287 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                9.56e-129      Length:          1023
Score:                    1420.00        Matches:         275
Percent Similarity:       90.72%         Conservative:    28
Best Local Similarity:    82.34%         Mismatches:      31
Query Match:              82.46%         Indels:          0
DB:                       10             Gaps:            0

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Qy          5 AsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeuAlaIleThrLeu 24
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 AACGCTTCTATGACAGTTATCGGTGCCGGTTCATACGGCACCGCTTTAGCGATTACCTTA 72

Qy         25 AlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHisIleAlaThrLeu 44
              ||||||||||||||:::|||||||||||||||||||||||||:::|||:::|||   |||
Db         73 GCGCGTAATGGGCACGATGTTGTGCTGTGGGGGCATGATCCCAAGCACGTTGCGGCATTA 132

Qy         45 GluArgAspArgCysAsnAlaAlaPheLeuProAspValProPheProAspThrLeuHis 64
              |||:::   |||||||||   |||||||||||||||||   ||||||||:::|||:::
Db        133 GAACAAGCGCGCTGTAATCAAGCCTTTCTGCCTGATGTTTCCTTTCCTGATAGTTTATAT 192

Qy         65 LeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeuValValValPro 84
              :::|||:::   |||      |||:::   ||||||||||||||||||||||:::|||
Db        193 ATGGAAGCTTCTTTGCAAAAAGCGATTGAAGCGAGCCGTAATATTCTTGTGGTGATCCCA 252

Qy         85 SerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArgProAspAlaArg 104
              ||||||||||||||||||||||:::||||||||||||   :::|||   |||||||||
Db        253 AGCCATGTGTTTGGTGAAGTACTGCAACAAATCAAACCCTTTTTACGTCAGGATGCGCGT 312

Qy        105 LeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeuGlnAspValAla 124
              :::|||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        313 GTTGTTTGGGCGACAAAAGGTCTTGAAGCACATACTGGTCGCTTATTACAAGATGTTGCC 372

Qy        125 ArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyProThrPheAlaLys 144
              ||||||   ||||||::::::|||||||||||||||:::|||||||||||||||||||||
Db        373 CGTGAAGTATTAGGTAATGAAATCCCGCTCGCAGTATTATCTGGCCCTACTTTTGCTAAA 432

Qy        145 GluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAspGlnThrPheAla 164
              ||||||||||||||||||||||||||||||::::::|||||||||||||   |||
Db        433 GAGCTTGCCGCGGGTTTGCCCACCGCGATTGCAGTGGCCTCGACGGATAATCTCTTTTTA 492

Qy        165 AspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyrSerAsnProAsp 184
              :::   ||||||||||||   |||||||||||||||||||||||||||   |||||||||
Db        493 GAGCAGTTACAACAGCTATTTCATTGTGGTAAAAGTTTCCGAGTCTATAAAAACCCTGAT 552

Qy        185 PheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIleGlyAlaGlyMet 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 TTTATCGGTGTGCAACTGGGTGGCGCTGTTAAAAACGTGATTGCTATTGGTGCGGGTATG 612

Qy        205 SerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThrArgGlyLeuAla 224
              ||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 TCTGATGGTATGGGATTTGGCGCTAATGCGCGTACCGCACTGATTACCCGAGGTCTAGCC 672

Qy        225 GluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPheMetGlyMetAla 244
              ||||||||||||||||   ||||||||||||||   ||||||||||||||||||||||
Db        673 GAAATGAGCCGTTTAGGTAAAGCCTTAGGTGCAGATGCGGCAACTTTTATGGGCATGGCT 732

Qy        245 GlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsnArgArgPheGly 264
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db        733 GGTTTGGGTGATTTAGTTTTAACCTGTACTGACAACCAATCACGTAATCGTCGCTTCGGT 792

Qy        265 MetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIleGlyGlnValVal 284
              ||||||||||||||||||:::||||||   :::|||||||||||||||||||||||||||
Db        793 ATGATGCTAGGTCAAGGTTTAGATGTTGATACAGCCCAAGAGAAAATTGGCCAGGTAGTC 852

Qy        285 GluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPheGlyValGluMet 304
              ||||||||||||||||||||||||||||||   ||||||   :::   ||||||||||||
Db        853 GAAGGTTATCGTAACACCAAAGAAGTTCGCGCATTAGCCGAACAGGTGGGTGTAGAAATG 912

Qy        305 ProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAlaArgGluAlaAla 324
              ||||||||||||:::|||||||||:::||||||      |||:::   :::||||||||||
Db        913 CCAATCACCGAACAGATCTACCAAATTTTATATCAACATAAAGATGTAAAAGAGGCTGCA 972

Qy        325 LeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSer 338
              |||   ||||||||||||||   |||||||||      |||
Db        973 TTGGCTTTATTAGGGCGAGCAACCAAAGATGAGATAGACAGC 1014

RESULT 12
ACA44463
ID   ACA44463 standard; DNA; 1011 BP.
XX
AC   ACA44463;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #26120.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Proteus sp.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
```

XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU40593.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 32333; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1011 BP; 260 A; 206 C; 261 G; 284 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.1e-128	Length:	1011
Score:	1411.00	Matches:	274
Percent Similarity:	90.12%	Conservative:	27
Best Local Similarity:	82.04%	Mismatches:	33
Query Match:	81.94%	Indels:	0
DB:	8	Gaps:	0

US-10-088-079-2 (1-339) x ACA44463 (1-1011)

```
Qy          5 AsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeuAlaIleThrLeu 24
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 AACGCTTCTATGACAGTTATCGGTGCCGGTTCATACGGCACCGCTTTAGCGATTACCTTA 63

Qy         25 AlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHisIleAlaThrLeu 44
              ||||||||||||||:::|||||||||||||||||||||||||:::|||:::|||   |||
Db         64 GCGCGTAATGGGCACGATGTTGTGCTGTGGGGGCATGATCCCAAGCACGTTGCGGCATTA 123

Qy         45 GluArgAspArgCysAsnAlaAlaPheLeuProAspValProPheProAspThrLeuHis 64
              |||:::  ||||||||  |||||||||||||||||  |||||||||:::|||:::
Db        124 GAACAAGCGCGCTGTAATCAAGCCTTTCTGCCCGATGTTTCCTTTCCTGATAGTTTATAT 183

Qy         65 LeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeuValValValPro 84
              :::|||:::  |||     |||:::  ||||||||||||||||||||||:::|||
Db        184 ATGGAAGCTTCTTTGCAAAAAGCGATTGAAGCGAGCCGTAATATTCTTGTGGTGATCCCA 243

Qy         85 SerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArgProAspAlaArg 104
              |||||||||||||||||||||||:::|||||||||||   :::|||  ||||||||
Db        244 AGCCATGTGTTTGGTGAAGTACTGCAACAAATCAAACCCTTTTTACGTCAGGATGCGCGT 303

Qy        105 LeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeuGlnAspValAla 124
              :::|||||||||||||||||||||||||  ||||||||||||||||||||||
Db        304 GTTGTTTGGGCGACAAAAGGTCTTGAAGCACATACTGGTCGCTTATTACAAGATGTTGCC 363

Qy        125 ArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyProThrPheAlaLys 144
              ||||||  ||||||:::::|||||||||||||||:::|||||||||||||||||||||
Db        364 CGTGAAGTATTAGGTAATGAAATCCCGCTCGCAGTATTATCTGGCCCTACTTTTGCTAAA 423

Qy        145 GluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAspGlnThrPheAla 164
              ||||||||||||||||||||||||||||||:::::|||||||||||   |||
Db        424 GAGCTTGCAGCGGGTTTACCCACCGCGATTGCAGTGGCCTCGACGGATAATCTCTTTTTA 483

Qy        165 AspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyrSerAsnProAsp 184
              :::  ||||||||||||  |||||||||||||||||||||||  ||||||||
Db        484 GAACAGTTACAACAGCTATTTCATTGTGGTAAAAGCTTCCGAGTCTATAAAAACCCTGAT 543

Qy        185 PheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIleGlyAlaGlyMet 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 TTTATCGGTGTGCAACTGGGGGGCGCTGTTAAAAACGTGATTGCTATTGGTGCGGGTATG 603

Qy        205 SerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThrArgGlyLeuAla 224
              |||||||||:::|||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTGATGGTATGGGATTTGGCGCTAATGCGCGTACTGCACTTATTACCCGTGGTCTGGCC 663

Qy        225 GluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPheMetGlyMetAla 244
              ||||||||||||||||  ||||||||||||||  ||||||||||||||||||||
Db        664 GAAATGAGCCGCTTAGGTAAAGCCTTAGGTGCAGATGCGGCAACTTTTATGGGCATGGCT 723

Qy        245 GlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsnArgArgPheGly 264
              ||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        724 GGTTTGGGTGATTTAGTTTTAACCTGTACTGACAACCAATCACGTAATCGTCGCTTCGGT 783

Qy        265 MetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIleGlyGlnValVal 284
              |||||||||||||||||  |||  :::|||||||||||||||||||||||||||||||
Db        784 ATGATGCTAGGTCAAGGTTTTGGTGTTGATACAGCCCAAGAGAAAATTGGCCAGGTAGTC 843

Qy        285 GluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPheGlyValGluMet 304
              ||||||||||||||||||||||||||||  ||||||  :::  ||||||||||||
Db        844 GAAGGTTATCGTAACACCAAAGAAGTTCGCGCATTAGCCGAACAGGTGGGTGTAGAAATG 903

Qy        305 ProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAlaArgGluAlaAla 324
              ||||||||||||:::|||||||||:::||||||      |||:::   :::||||||||||
Db        904 CCAATCACCGAACAGATCTACCAAATTTTATATCAACATAAAGATGTAAAAGAGGCTGCA 963

Qy        325 LeuThrLeuLeuGlyArgAlaArgLysAspGluArgSerSer 338
              |||   ||||||||||||||   |||||||||      |||
Db        964 TTGGCTTTATTAGGGCGAGCAACCAAAGATGAGATAGACAGC 1005
```

RESULT 13
ACF70491
ID ACF70491 standard; DNA; 1023 BP.
XX
AC ACF70491;
XX
DT 20-NOV-2003 (first entry)
XX
DE Photorhabdus luminescens nucleotide sequence #8958.
XX
KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough; gene; ds.
XX
OS Photorhabdus luminescens.
XX
PN WO200294867-A2.
XX
PD 28-NOV-2002.
XX

PF 07-FEB-2002; 2002WO-IB003040.
XX
PR 07-FEB-2001; 2001FR-00001659.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
DR WPI; 2003-148459/14.
XX
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 2; SEQ ID NO 8958; 1205pp; French.
XX
CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes
XX
SQ Sequence 1023 BP; 260 A; 197 C; 275 G; 291 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.66e-126	Length:	1023
Score:	1393.50	Matches:	270
Percent Similarity:	89.55%	Conservative:	30
Best Local Similarity:	80.60%	Mismatches:	34
Query Match:	80.92%	Indels:	1
DB:	10	Gaps:	1

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Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||                ||||||||||||||||||||||||||||||||:::|||
Db          1 ATGAATAGT---ACTGTTTCTATGACAGTGATTGGTGCCGGCTCATACGGCACCTCATTA 57

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||    ||||||||||||||||:::|||||||||
Db         58 GCCATTACGCTGGCTCGTAATGGTCATAATGTTGTACTTTGGGGGCATAATCCAGAGCAT 117

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              :::      |||:::|||   |||||||||      ||||||||||||||   ||||||
Db        118 GTTGGGGCATTGCAACGGGTGCGTTGTAATCAAAAATTTCTGCCGGATGTTTCCTTTCCT 177

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              |||:::|||   ||||||:::||||||      ||||||   |||||||||:::||||||
Db        178 GATAGTTTATTGCTTGAAACGGACCTAATAAAAGCACTAACAGCGAGCCGCGATATTCTT 237

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||||||||||:::||||||||||||   :::|||
Db        238 GTTGTGGTACCTAGCCATGTGTTTGGTGAAGTGTTAAAGCAGATAAAACCACATTTACGG 297

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||:::|||:::||||||||||||||||||||||||||:::||||||||||||||||
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```
Db        298 CCTGATTCACGTATCGTATGGGCAACTAAAGGCTTGGAAGCGGATACCGGTCGGTTATTG 357

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||||    ||||||:::::||||||||||||||||:::||||||||||
Db        358 CAGGATGTGGCCCGTGAGATATTAGGCAATGAAATACCGCTAGCGGTGCTCTCTGGGCCA 417

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||:::::::::::|||:::
Db        418 ACATTTGCTAAAGAGTTAGCGGCTGGTTTGCCTACCGCGATTGCTATTTCCGCGACGGAA 477

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
                    |||   |||   ||||||||||||   ||||||||||||||||||||||||||||
Db        478 TCTGCTTTTGGCGATGGACTTCAACAATTATTCCACTGTGGCAAAAGTTTCCGGGTTTAT 537

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AAAAATCCTGATTTTATTGGTGTTCAACTCGGTGGTGCCGTAAAAAACGTGATCGCCATT 597

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              |||||||||:::|||||||||:::|||||||||||||||||||||||||||||||||||
Db        598 GGCGCGGGAATATCTGATGGCATGGGATTTGGTGCTAATGCTCGTACCGCATTGATTACT 657

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        658 CGTGGATTGGCGGAAATGAGTCGCCTTGGTGCAGCGCTTGGTGCTGATCCTTCTACCTTT 717

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              |||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        718 ATGGGCATGGCGGGATTGGGCGATTTGGTCTTAACTTGTACTGATAACCAATCACGTAAC 777

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||:::   |||:::   ||||||   :::|||
Db        778 CGTCGTTTTGGCATGATGCTGGGGCAGGGAATCAGTGTTGAAGAAGCGCAGTATCAGATT 837

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||   ||||||:::|||
Db        838 GGGCAGGTTGTTGAAGGTTATCGCAATACCAAAGAAGTACGTGCATTGGCTAATCGCGCC 897

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
                 |||||||||||||||   |||:::|||||||||:::|||||||||   ||||||
Db        898 AATGTAGAAATGCCGATTGCAGAACAAATCTACCAGATACTCTATTGCAATAAAAATGTG 957

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGlu 335
                 |||||||||      ||||||||||||||||||||||||||
Db        958 ATAGAAGCTGCTCAGGCATTATTAGGAAGAGCCAGAAAGGATGAG 1002
```

RESULT 14
ACF65374
ID ACF65374 standard; DNA; 69727 BP.
XX
AC ACF65374;
XX
DT 20-NOV-2003 (first entry)
XX
DE Photorhabdus luminescens nucleotide sequence #27.
XX
KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough; gene; ds.
XX
OS Photorhabdus luminescens.
XX
PN WO200294867-A2.
XX
PD 28-NOV-2002.
XX
PF 07-FEB-2002; 2002WO-IB003040.
XX
PR 07-FEB-2001; 2001FR-00001659.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.

XX
PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
DR WPI; 2003-148459/14.
XX
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 1; SEQ ID NO 27; 1205pp; French.
XX
CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes
XX
SQ Sequence 69727 BP; 20213 A; 13239 C; 14632 G; 21638 T; 0 U; 5 Other;

Alignment Scores:

Pred. No.:	9.67e-124	Length:	69727
Score:	1393.50	Matches:	270
Percent Similarity:	89.55%	Conservative:	30
Best Local Similarity:	80.60%	Mismatches:	34
Query Match:	80.92%	Indels:	1
DB:	10	Gaps:	1

US-10-088-079-2 (1-339) x ACF65374 (1-69727)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||              ||||||||||||||||||||||||||||||:::|||
Db      54175 ATGAATAGT---ACTGTTTCTATGACAGTGATTGGTGCCGGCTCATACGGCACCTCATTA 54231

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||    ||||||||||||||||:::|||||||||
Db      54232 GCCATTACGCTGGCTCGTAATGGTCATAATGTTGTACTTTGGGGGCATAATCCAGAGCAT 54291

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              :::      |||:::|||   |||||||||     ||||||||||||||   ||||||
Db      54292 GTTGGGGCATTGCAACGGGTGCGTTGTAATCAAAAATTTCTGCCGGATGTTTCCTTTCCT 54351

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              |||:::|||   ||||||:::||||||      ||||||   |||||||||:::||||||
Db      54352 GATAGTTTATTGCTTGAAACGGACCTAATAAAAGCACTAACAGCGAGCCGCGATATTCTT 54411

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||||||||:::|||||||||||   :::|||
Db      54412 GTTGTGGTACCTAGCCATGTGTTTGGTGAAGTGTTAAAGCAGATAAAACCACATTTACGG 54471

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||:::|||:::|||||||||||||||||||||||:::|||||||||||||||
Db      54472 CCTGATTCACGTATCGTATGGGCAACTAAAGGCTTGGAAGCGGATACCGGTCGGTTATTG 54531

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||   ||||||::::::|||||||||||||||:::|||||||||
Db      54532 CAGGATGTGGCCCGTGAGATATTAGGCAATGAAATACCGCTAGCGGTGCTCTCTGGGCCA 54591

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||||||||:::::::::::|||:::
Db      54592 ACATTTGCTAAAGAGTTAGCGGCTGGTTTGCCTACCGCGATTGCTATTTCCGCGACGGAA 54651

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
                  |||   |||   ||||||||||||   |||||||||||||||||||||||||
Db      54652 TCTGCTTTTGGCGATGGACTTCAACAATTATTCCACTGTGGCAAAAGTTTCCGGGTTTAT 54711

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      54712 AAAAATCCTGATTTTATTGGTGTTCAACTCGGTGGTGCCGTAAAAAACGTGATCGCCATT 54771

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              |||||||:::|||||||:::||||||||||||||||||||||||||||||||||||
Db      54772 GGCGCGGGAATATCTGATGGCATGGGATTTGGTGCTAATGCTCGTACCGCATTGATTACT 54831

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db      54832 CGTGGATTGGCGGAAATGAGTCGCCTTGGTGCAGCGCTTGGTGCTGATCCTTCTACCTTT 54891

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db      54892 ATGGGCATGGCGGGATTGGGCGATTTGGTCTTAACTTGTACTGATAACCAATCACGTAAC 54951

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              |||||||||||||||||||||||||||||:::   |||:::   ||||||   :::|||
Db      54952 CGTCGTTTTGGCATGATGCTGGGGCAGGGAATCAGTGTTGAAGAAGCGCAGTATCAGATT 55011

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||||   ||||||:::|||
Db      55012 GGGCAGGTTGTTGAAGGTTATCGCAATACCAAAGAAGTACGTGCATTGGCTAATCGCGCC 55071

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||||   |||:::|||||||||:::|||||||||   ||||||
Db      55072 AATGTAGAAATGCCGATTGCAGAACAAATCTACCAGATACTCTATTGCAATAAAAATGTG 55131

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGlu 335
              |||||||||       ||||||||||||||||||||||||||
Db      55132 ATAGAAGCTGCTCAGGCATTATTAGGAAGAGCCAGAAAGGATGAG 55176
```

RESULT 15
ACF67367_35
Continuation (36 of 57) of ACF67367 from base 3500001 (Photorhabdus luminescens nucleoti
WP Sequence split into 57 fragments LOCUS ACF67367 Accession Acf67367

WP	Fragment Name	Begin	End
WP	ACF67367_00	1	110000
WP	ACF67367_01	100001	210000
WP	ACF67367_02	200001	310000
WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
WP	ACF67367_10	1000001	1110000
WP	ACF67367_11	1100001	1210000
WP	ACF67367_12	1200001	1310000
WP	ACF67367_13	1300001	1410000
WP	ACF67367_14	1400001	1510000
WP	ACF67367_15	1500001	1610000
WP	ACF67367_16	1600001	1710000
WP	ACF67367_17	1700001	1810000
WP	ACF67367_18	1800001	1910000
WP	ACF67367_19	1900001	2010000
WP	ACF67367_20	2000001	2110000
WP	ACF67367_21	2100001	2210000
WP	ACF67367_22	2200001	2310000
WP	ACF67367_23	2300001	2410000
WP	ACF67367_24	2400001	2510000
WP	ACF67367_25	2500001	2610000
WP	ACF67367_26	2600001	2710000
WP	ACF67367_27	2700001	2810000

WP	ACF67367_28	2800001	2910000
WP	ACF67367_29	2900001	3010000
WP	ACF67367_30	3000001	3110000
WP	ACF67367_31	3100001	3210000
WP	ACF67367_32	3200001	3310000
WP	ACF67367_33	3300001	3410000
WP	ACF67367_34	3400001	3510000
WP	ACF67367_35	3500001	3610000
WP	ACF67367_36	3600001	3710000
WP	ACF67367_37	3700001	3810000
WP	ACF67367_38	3800001	3910000
WP	ACF67367_39	3900001	4010000
WP	ACF67367_40	4000001	4110000
WP	ACF67367_41	4100001	4210000
WP	ACF67367_42	4200001	4310000
WP	ACF67367_43	4300001	4410000
WP	ACF67367_44	4400001	4510000
WP	ACF67367_45	4500001	4610000
WP	ACF67367_46	4600001	4710000
WP	ACF67367_47	4700001	4810000
WP	ACF67367_48	4800001	4910000
WP	ACF67367_49	4900001	5010000
WP	ACF67367_50	5000001	5110000
WP	ACF67367_51	5100001	5210000
WP	ACF67367_52	5200001	5310000
WP	ACF67367_53	5300001	5410000
WP	ACF67367_54	5400001	5510000
WP	ACF67367_55	5500001	5610000
WP	ACF67367_56	5600001	5648894

Alignment Scores:

Pred. No.:	1.77e-123	Length:	110000
Score:	1393.50	Matches:	270
Percent Similarity:	89.55%	Conservative:	30
Best Local Similarity:	80.60%	Mismatches:	34
Query Match:	80.92%	Indels:	1
DB:	10	Gaps:	1

US-10-088-079-2 (1-339) x ACF67367_35 (1-110000)

```
Qy          1 MetAsnGlnArgAsnAlaSerMetThrValIleGlyAlaGlySerTyrGlyThrAlaLeu 20
              ||||||           |||||||||||||||||||||||||||||||||||:::|||
Db      79826 ATGAATAGT---ACTGTTTCTATGACAGTGATTGGTGCCGGCTCATACGGCACCTCATTA 79882

Qy         21 AlaIleThrLeuAlaArgAsnGlyHisGluValValLeuTrpGlyHisAspProGluHis 40
              ||||||||||||||||||||||||   ||||||||||||||||||:::||||||||||
Db      79883 GCCATTACGCTGGCTCGTAATGGTCATAATGTTGTACTTTGGGGGCATAATCCAGAGCAT 79942

Qy         41 IleAlaThrLeuGluArgAspArgCysAsnAlaAlaPheLeuProAspValProPhePro 60
              :::      |||:::|||   |||||||||      ||||||||||||||   ||||||
Db      79943 GTTGGGGCATTGCAACGGGTGCGTTGTAATCAAAAATTTCTGCCGGATGTTTCCTTTCCT 80002

Qy         61 AspThrLeuHisLeuGluSerAspLeuAlaThrAlaLeuAlaAlaSerArgAsnIleLeu 80
              |||:::|||   ||||||:::|||||||      ||||||   |||||||||:::||||||
Db      80003 GATAGTTTATTGCTTGAAACGGACCTAATAAAAGCACTAACAGCGAGCCGCGATATTCTT 80062

Qy         81 ValValValProSerHisValPheGlyGluValLeuArgGlnIleLysProLeuMetArg 100
              ||||||||||||||||||||||||||||||||||:::||||||||||||   :::|||
Db      80063 GTTGTGGTACCTAGCCATGTGTTTGGTGAAGTGTTAAAGCAGATAAAACCACATTTACGG 80122

Qy        101 ProAspAlaArgLeuValTrpAlaThrLysGlyLeuGluAlaGluThrGlyArgLeuLeu 120
              ||||||:::|||:::|||||||||||||||||||||||||||:::|||||||||||||||
Db      80123 CCTGATTCACGTATCGTATGGGCAACTAAAGGCTTGGAAGCGGATACCGGTCGGTTATTG 80182

Qy        121 GlnAspValAlaArgGluAlaLeuGlyAspGlnIleProLeuAlaValIleSerGlyPro 140
              ||||||||||||||||   ||||||::::::|||||||||||||||:::|||||||||
Db      80183 CAGGATGTGGCCCGTGAGATATTAGGCAATGAAATACCGCTAGCGGTGCTCTCTGGGCCA 80242

Qy        141 ThrPheAlaLysGluLeuAlaAlaGlyLeuProThrAlaIleSerLeuAlaSerThrAsp 160
              ||||||||||||||||||||||||||||||||||||:::::::::::|||:::
Db      80243 ACATTTGCTAAAGAGTTAGCGGCTGGTTTGCCTACCGCGATTGCTATTTCCGCGACGGAA 80302

Qy        161 GlnThrPheAlaAspAspLeuGlnGlnLeuLeuHisCysGlyLysSerPheArgValTyr 180
```

```
                  |||   |||   ||||||||||||   ||||||||||||||||||||||||||||
Db      80303 TCTGCTTTTGGCGATGGACTTCAACAATTATTCCACTGTGGCAAAAGTTTCCGGGTTTAT 80362

Qy        181 SerAsnProAspPheIleGlyValGlnLeuGlyGlyAlaValLysAsnValIleAlaIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80363 AAAAATCCTGATTTTATTGGTGTTCAACTCGGTGGTGCCGTAAAAAACGTGATCGCCATT 80422

Qy        201 GlyAlaGlyMetSerAspGlyIleGlyPheGlyAlaAsnAlaArgThrAlaLeuIleThr 220
              ||||||||:::||||||||:::||||||||||||||||||||||||||||||||||||
Db      80423 GGCGCGGGAATATCTGATGGCATGGGATTTGGTGCTAATGCTCGTACCGCATTGATTACT 80482

Qy        221 ArgGlyLeuAlaGluMetSerArgLeuGlyAlaAlaLeuGlyAlaAspProAlaThrPhe 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db      80483 CGTGGATTGGCGGAAATGAGTCGCCTTGGTGCAGCGCTTGGTGCTGATCCTTCTACCTTT 80542

Qy        241 MetGlyMetAlaGlyLeuGlyAspLeuValLeuThrCysThrGluAsnGlnSerArgAsn 260
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db      80543 ATGGGCATGGCGGGATTGGGCGATTTGGTCTTAACTTGTACTGATAACCAATCACGTAAC 80602

Qy        261 ArgArgPheGlyMetMetLeuGlyGlnGlyMetAspValGlnSerAlaGlnGluLysIle 280
              ||||||||||||||||||||||||||:::   |||:::   ||||||   :::|||
Db      80603 CGTCGTTTTGGCATGATGCTGGGGCAGGGAATCAGTGTTGAAGAAGCGCAGTATCAGATT 80662

Qy        281 GlyGlnValValGluGlyTyrArgAsnThrLysGluValArgGluLeuAlaHisArgPhe 300
              ||||||||||||||||||||||||||||||||||||||   ||||||:::|||
Db      80663 GGGCAGGTTGTTGAAGGTTATCGCAATACCAAAGAAGTACGTGCATTGGCTAATCGCGCC 80722

Qy        301 GlyValGluMetProIleThrGluGluIleTyrGlnValLeuTyrCysGlyLysAsnAla 320
              ||||||||||||||   |||:::||||||||:::||||||||   ||||||
Db      80723 AATGTAGAAATGCCGATTGCAGAACAAATCTACCAGATACTCTATTGCAATAAAAATGTG 80782

Qy        321 ArgGluAlaAlaLeuThrLeuLeuGlyArgAlaArgLysAspGlu 335
                    |||||||||      ||||||||||||||||||||||||
Db      80783 ATAGAAGCTGCTCAGGCATTATTAGGAAGAGCCAGAAAGGATGAG 80827
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Search completed: April 27, 2005, 15:42:11
Job time : 772 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2005, 10:44:58 ; Search time 164 Seconds
(without alignments)
799.462 Million cell updates/sec

Title: US-10-088-079-2
Perfect score: 1722
Sequence: 1 MNQRNASMTVIGAGSYGTAL.....AREAALTLLGRARKDERSSH 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1722	100.0	339	4	AAB62189	Aab62189 E. coli g
2	1719	99.8	339	2	AAW57330	Aaw57330 Glycerol-
3	1719	99.8	339	2	AAW60258	Aaw60258 Klebsiell
4	1719	99.8	339	2	AAY26172	Aay26172 Glycerol-
5	1719	99.8	339	4	AAU34796	Aau34796 E. coli c
6	1719	99.8	339	6	ABU28819	Abu28819 Protein e
7	1719	99.8	339	8	ADS45174	Ads45174 Bacterial
8	1640	95.2	339	6	ABU47465	Abu47465 Protein e
9	1635	94.9	339	6	ABU28096	Abu28096 Protein e
10	1621	94.1	339	6	ABU45354	Abu45354 Protein e
11	1587	92.2	339	6	ABU31968	Abu31968 Protein e
12	1587	92.2	345	7	ABO64223	Abo64223 Klebsiell
13	1455	84.5	339	6	ABU50149	Abu50149 Protein e
14	1420	82.5	340	7	ADF07218	Adf07218 Bacterial
15	1411	81.9	337	6	ABU40593	Abu40593 Protein e
16	1393.5	80.9	341	6	ABM68792	Abm68792 Photorhab
17	1373	79.7	330	8	ADN17703	Adn17703 Bacterial
18	1372	79.7	330	8	ADS42893	Ads42893 Bacterial
19	1242	72.1	344	6	ABU49620	Abu49620 Protein e
20	1192	69.2	337	6	ABU39371	Abu39371 Protein e
21	1150	66.8	335	4	AAU35472	Aau35472 Haemophil
22	1150	66.8	335	6	ABU30312	Abu30312 Protein e
23	806	46.8	329	6	ABU33190	Abu33190 Protein e
24	794.5	46.1	334	8	ADS26951	Ads26951 Bacterial
25	794.5	46.1	334	8	ADS27309	Ads27309 Bacterial
26	794.5	46.1	340	8	ADS26576	Ads26576 Bacterial
27	751.5	43.6	346	8	ADS28582	Ads28582 Bacterial
28	738.5	42.9	334	8	ADN26503	Adn26503 Bacterial
29	720.5	41.8	334	8	ADS27486	Ads27486 Bacterial
30	709.5	41.2	340	6	ABU18125	Abu18125 Protein e
31	703	40.8	332	6	ABU23655	Abu23655 Protein e
32	694	40.3	343	6	ABU25613	Abu25613 Protein e
33	692	40.2	355	6	ABU30030	Abu30030 Protein e
34	692	40.2	356	7	ADC94377	Adc94377 E. faeciu
35	681	39.5	353	7	ADC95426	Adc95426 E. faeciu
36	677.5	39.3	339	6	ADB08818	Adb08818 Alloiococ
37	677.5	39.3	342	6	ADB08820	Adb08820 Alloiococ
38	673	39.1	340	4	AAU35259	Aau35259 Enterococ
39	673	39.1	340	6	ABU14598	Abu14598 Protein e
40	672.5	39.1	338	5	ABB49213	Abb49213 Listeria
41	672.5	39.1	338	6	ABU32661	Abu32661 Protein e
42	672.5	39.1	342	4	AAU33428	Aau33428 Enterococ
43	666.5	38.7	327	6	ADB08816	Adb08816 Alloiococ
44	666.5	38.7	345	8	ADS44752	Ads44752 Bacterial
45	666	38.7	335	6	ABU17729	Abu17729 Protein e

ALIGNMENTS

RESULT 1
AAB62189
ID AAB62189 standard; protein; 339 AA.
XX
AC AAB62189;
XX
DT 11-JUN-2001 (first entry)
XX
DE E. coli gpsA2FR protein.
XX
KW Glycerol-3-phosphate dehydrogenase; G3PD; feedback inhibition; oil seed;
KW genetic transformation; fatty acid; glycerolipid; osmotic stress; gpsA;
KW gpsA2FR; allele.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
FT Misc-difference 255
FT /label= D255E
FT /note= "wild-type Asp is replaced with Glu"
XX
PN WO200121820-A1.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-CA001096.
XX
PR 22-SEP-1999; 99US-0155133P.
XX
PA (CANA) NAT RES COUNCIL CANADA.
XX
PI Zou J, Wei Y, Periappuram C; Selvaraj G, Datla R;
XX
DR WPI; 2001-257996/26.
DR N-PSDB; AAF57428.
XX
PT Manipulating glycerol-3-phosphate metabolism of plant for enhancing
PT stress tolerance, altering fatty acid content in glycerolipids, by
PT expressing in plant feedback defective glycerol-3-phosphate dehydrogenase
PT gene.
XX
PS Claim 15; Fig 1; 39pp; English.
XX
CC The invention provides a method for genetically transforming a plant so
CC that it expresses a a heterologous glycerol-3-phosphate dehydrogenase
CC (G3PD) that is less sensitive to feedback inhibition than wild-type G3PD.
CC The method involves providing a vector comprising a DNA sequence encoding
CC G3PD that is less sensitive to feedback inhibition than wild-type G3PD

CC and transforming the plant with the vector. The method is useful for
CC expressing a heterologous G3PD less sensitive to feedback inhibition than
CC wild-type G3PD in an oil seed bearing plant, such as Arabidopsis thaliana
CC or Brassica. The vectors are useful for producing a genetically altered
CC plant having altered fatty acid content in its glycerolipids, especially
CC elevated levels of C16 fatty acids and increased osmotic stress tolerance
CC relative to the wild type. The present sequence represents the E. coli
CC gpsA2FR protein. The gene gpsA2FR is an allele of the E. coli gpsA gene,
CC and encodes an altered version of the GPDH protein defective in feedback
CC inhibition. This gpsA2FR gene can be used in the vectors and method of
CC the invention
XX
SQ Sequence 339 AA;

Query Match 100.0%; Score 1722; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.2e-159;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
```

RESULT 2
AAW57330
ID AAW57330 standard; protein; 339 AA.
XX
AC AAW57330;
XX
DT 14-SEP-1998 (first entry)
XX
DE Glycerol-3-phosphate dehydrogenase gpsA.
XX
KW Glycerol-3-phosphate dehydrogenase; G3PDH; gpsA; yeast.
XX
OS Saccharomyces sp.
XX
PN WO9821340-A1.
XX
PD 22-MAY-1998.
XX
PF 10-NOV-1997; 97WO-US020293.
XX
PR 13-NOV-1996; 96US-0030602P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (GEMV) GENENCOR INT INC.
XX
PI Bulthuis BA, Gatenby AA, Haynie SL, Hsu AK, Lareau RD;
XX
DR WPI; 1998-297943/26.
XX
PT Fermentative production of glycerol using recombinant host - containing
PT genes for glycerol-3-phosphate dehydrogenase and-or glycerol-3-
PT phosphatase.
XX
PS Claim 9; Page 36-37; 57pp; English.
XX
CC This claimed Saccharomyces polypeptide comprises a glycerol-3-phosphate
CC dehydrogenase (G3PDH) that catalyses the conversion of dihydroxyacetone
CC phosphate to glycerol-3-phosphate. It is encoded by the gpsA gene. The
CC invention provides recombinant organisms that express G3PDH and/or
CC glycerol-3-phosphatase (G3P) (see also AAW57324-32) useful for the
CC production of glycerol from a variety of C-sources. A host cell is
CC preferably transformed with a cassette containing either a G3PDH gene
CC and/or a G3P gene and then cultured in the presence of a mono-, oligo-,
CC polysaccharide or 1C-substrate. The glycerol obtained is used in
CC cosmetics, liquid soaps, pharmaceuticals, lubricants and antifreezes; its
CC esters are used in the oil and fat industries. The method produces
CC glycerol rapidly and inexpensively without generation of polluting by-
CC products
XX
SQ Sequence 339 AA;

Query Match 99.8%; Score 1719; DB 2; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.4e-158;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
```

RESULT 3
AAW60258
ID AAW60258 standard; protein; 339 AA.
XX
AC AAW60258;
XX
DT 28-SEP-1998 (first entry)
XX
DE Klebsiella pneumoniae glycerol-3-phosphate dehydrogenase.
XX
KW glycerol-3-phosphate dehydrogenase; production; 1,3-propanediol;
KW recombinant.
XX
OS Klebsiella pneumoniae.
XX
PN WO9821341-A2.
XX
PD 22-MAY-1998.
XX
PF 13-NOV-1997; 97WO-US020873.
XX
PR 13-NOV-1996; 96US-0030601P.
XX

PA (GEMV) GENENCOR INT INC.
XX
PI Dunn-Coleman NS, Diaz-Torres M, Chase MW, Trimbur D;
XX
DR WPI; 1998-297944/26.
XX
PT New method for increasing production of 1,3-propane:diol - comprises
PT fermentation of inexpensive carbon sources by microorganism expressing
PT dehydratase, used, e.g. to prolong half-life of enzyme.
XX
PS Disclosure; Page 70-71; 133pp; English.
XX
CC The sequence is that of glycerol-3-phosphate dehydrogenase. It was used
CC as part of a method of fermentative production of 1,3-propanediol (1,3-
CC pd), using an organism comprising at least 1 gene encoding a dehydratase,
CC is improved by inserting into the host a gene encoding protein X and
CC culturing the transformant in presence of a carbon source (e.g. mono-,
CC oligo- or poly-saccharide or 1C substrate) convertible to 1,3-pd. 1,3-pd
CC is a starting material for polyesters, polyurethanes and cyclic
CC compounds. 1,3-pd can now be produced by a single recombinant organism
CC from inexpensive carbon sources such as glucose (rather than costly
CC glycerol or dihydroxyacetone), rapidly and without causing pollution
XX
SQ Sequence 339 AA;

Query Match 99.8%; Score 1719; DB 2; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.4e-158;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
```

RESULT 4
AAY26172
ID AAY26172 standard; protein; 339 AA.
XX
AC AAY26172;
XX
DT 29-SEP-1999 (first entry)
XX
DE Glycerol-3-phosphate dehydrogenase encoded by gpsA gene.
XX
KW G3PDH; glycerol-3-phosphate dehydrogenase; NADPH-dependent enzyme;
KW EC 1.1.1.94; glycerol; recombinant organism; transformation; gpsA gene;
KW glycerol biosynthetic pathway; expression cassette; 1-3 propanediol;
KW pharmaceutical compound; antifreeze solution; lubricant; polyurethane;
KW cyclic compound; fat and oil industry; polyester fiber.
XX
OS Saccharomyces sp.
XX
PN WO9928480-A1.
XX
PD 10-JUN-1999.
XX
PF 02-DEC-1998; 98WO-US025551.
XX
PR 02-DEC-1997; 97US-00982783.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (GEMV) GENENCOR INT INC.
XX
PI Nair RV, Payne MS, Trimbur DE, Valle F;
XX
DR WPI; 1999-385384/32.
XX
PT Recombinant organisms containing G3PDH and or G3P phosphatase.
XX
PS Claim 12; Page 63-64; 84pp; English.
XX
CC The present sequence is a glycerol-3-phosphate dehydrogenase (G3PDH)
CC enzyme (EC 1.1.1.94) which is NADPH dependent, and catalyses the
CC conversion of dihydroxyacetone phosphate to glycerol-3-phosphate. This is
CC encoded by gps A gene. This is used to produce glycerol from a
CC recombinant organism by transforming a suitable host cell with an
CC expression cassette comprising either one or both of the genes encoding
CC G3PDH and G3P, where the host cell has disruptions in either glycerol
CC kinase or glycerol dehydrogenase endogenous genes to prevent their active
CC expression. The transformed host cell is cultured with a carbon source
CC and glycerol is recovered. Compounds derived from the glycerol
CC biosynthetic pathway like 1,3-propanediol can also be produced. The
CC method provides a rapid, inexpensive and environment-friendly source of
CC glycerol. Glycerol is used in cosmetics, food, pharmaceuticals,
CC lubricants, anti-freeze solutions, fat and oil industry etc. . 1,3 -
CC propanediol is used for the production of polyester fibers and the
CC manufacture of polyurethanes and cyclic compounds
XX
SQ Sequence 339 AA;

Query Match 99.8%; Score 1719; DB 2; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.4e-158;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
```

RESULT 5
AAU34796
ID AAU34796 standard; protein; 339 AA.
XX
AC AAU34796;
XX
DT 14-FEB-2002 (first entry)

```
XX
DE   E. coli cellular proliferation protein #377.
XX
KW   Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW   antibacterial; drug design.
XX
OS   Escherichia coli.
XX
PN   WO200170955-A2.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2001; 2001WO-US009180.
XX
PR   21-MAR-2000; 2000US-0191078P.
PR   23-MAY-2000; 2000US-0206848P.
PR   26-MAY-2000; 2000US-0207727P.
PR   23-OCT-2000; 2000US-0242578P.
PR   27-NOV-2000; 2000US-0253625P.
PR   22-DEC-2000; 2000US-0257931P.
PR   16-FEB-2001; 2001US-0269308P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Haselbeck R,  Ohlsen KL,  Zyskind JW,  Wall D,  Trawick JD,  Carr GJ;
PI   Yamamoto RT,  Xu HH;
XX
DR   WPI; 2001-611495/70.
DR   N-PSDB; AAS52655.
XX
PT   New polynucleotides for the identification and development of
PT   antibiotics, comprise sequences of antisense nucleic acids.
XX
PS   Example 3; SEQ ID NO 10389; 511pp; English.
XX
CC   The invention relates to antisense inhibitors of genes essential to
CC   prokaryotic cellular proliferation, their use in identifying the genes,
CC   their use in the discovery of novel antibiotics, the essential genes
CC   themselves and the encoded proteins. The prokaryotes used are Escherichia
CC   coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC   Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC   useful for the identification of potential new targets for antibiotic
CC   development. The antisense nucleic acids can also be used to identify
CC   proteins used in proliferation, to express these proteins, and to obtain
CC   antibodies capable of binding to the expressed proteins. The proteins can
CC   be used to screen compounds in rational drug discovery programmes. The
CC   antisense nucleic acid sequence is also useful to screen for homologous
CC   nucleic acids which are required for cell proliferation in a wide variety
CC   of organisms. The present sequence represents an essential prokaryotic
CC   cellular proliferation protein. Note: The sequence data for this patent
CC   did not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 339 AA;

  Query Match             99.8%;  Score 1719;  DB 4;  Length 339;
  Best Local Similarity   99.7%;  Pred. No. 1.4e-158;
  Matches  338;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339


RESULT 6
ABU28819
ID   ABU28819 standard; protein; 339 AA.
XX
AC   ABU28819;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Protein encoded by Prokaryotic essential gene #14346.
XX
KW   Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS   Escherichia coli.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   N-PSDB; ACA32689.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 25; SEQ ID NO 56743; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
```

CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 339 AA;

Query Match 99.8%; Score 1719; DB 6; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.4e-158;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
```

RESULT 7
ADS45174
ID ADS45174 standard; protein; 339 AA.
XX
AC ADS45174;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #23604.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 23604; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 339 AA;

Query Match 99.8%; Score 1719; DB 8; Length 339;
Best Local Similarity 99.7%; Pred. No. 1.4e-158;
Matches 338; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||||
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
```

RESULT 8
ABU47465
ID ABU47465 standard; protein; 339 AA.
XX

```
AC   ABU47465;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Protein encoded by Prokaryotic essential gene #32992.
XX
KW   Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS   Salmomella typhi.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   N-PSDB; ACA51335.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 25; SEQ ID NO 75389; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC   the target prokaryotic essential genes. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 339 AA;

  Query Match             95.2%;  Score 1640;  DB 6;  Length 339;
  Best Local Similarity   94.7%;  Pred. No. 7e-151;
  Matches  321;  Conservative    8;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||| |||||||||||||||||||||||:||||||:|||||| |||| |||||||||
Db          1 MNQSNASMTVIGAGSYGTALAITLARNGHQVVLWGHDPKHIATLEHDRCNVAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              |||||||||||||||||||||||||||| :|||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFSDVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDETFADDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              | |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        181 INADFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLTEMSRLGAALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:|||||||||||||||||: ||:|||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVKGAQDKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||:| | |
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKEELSRH 339


RESULT 9
ABU28096
ID   ABU28096 standard; protein; 339 AA.
XX
AC   ABU28096;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Protein encoded by Prokaryotic essential gene #13623.
XX
KW   Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS   Enterobacter cloacae.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   N-PSDB; ACA31966.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 25; SEQ ID NO 56020; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
```

CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 339 AA;

Query Match 94.9%; Score 1635; DB 6; Length 339;
Best Local Similarity 94.1%; Pred. No. 2.2e-150;
Matches 319; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              |:  |||||||||||||||||||||||||||||||||:|||||:||||| |||||||||
Db          1 MSTVNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPKHIATLQRDRCNVAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              |:|||||||||||||||||:||||||||:|||||||||||||||:|||||||||||||||
Db         61 DSLHLESDLATALAASRNILIVVPSHVFGDVLRQIKPLMRPDARIVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              |||||||||| |||||||||||||||||||||||||||| |:||||||||||||||||||
Db        121 QDVAREALGDAIPLAVISGPTFAKELAAGLPTAISLASTDQAFSDDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              |||||||||||||||||||||||||||||||||||||||||||| |||||| |||||||||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLTEMSRLGEALGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:|||||||||||||||| ||: |||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGSDVKGAQEKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||||||||:
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSN 339
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RESULT 10
ABU45354
ID ABU45354 standard; protein; 339 AA.
XX
AC ABU45354;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #30881.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Salmonella paratyphi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA49224.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 73278; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 339 AA;

Query Match 94.1%; Score 1621; DB 6; Length 339;
Best Local Similarity 93.8%; Pred. No. 5e-149;
Matches 318; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||| |||||||||||||| |||||||||:|||||||:|||||| |||| |||||||||
Db          1 MNQSNASMTVIGAGSYGTPLAITLARNGHQVVLWGHDPKHIATLEHDRCNVAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              |||||||||||||||||||||||||| :|||||||||||||||||||||||||||||||
Db         61 DTLHLESDLATALAASRNILVVVPSHVFSDVLRQIKPLMRPDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              |||||||||||||||||||||||||||| |||||||||:|||||||||||||||||||
Db        121 QDVAREALGDQIPLAVISGPTFAKELAAGLRTAISLASTDETFADDLQQLLHCGKSFRVY 180
```

```
Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              | |||||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||
Db        181 INADFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLTEMSRLGARLGADPATF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              ||||||||||||||:||||||||||||||||: ||:|||||||||||||||||||||||||
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVKGAQDKIGQVVEGYRNTKEVRELAHRF 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||||||||||||||||:| | |
Db        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKEELSRH 339
```

RESULT 11
ABU31968
ID ABU31968 standard; protein; 339 AA.
XX
AC ABU31968;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #17495.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Klebsiella pneumoniae.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA35838.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 59892; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 339 AA;

  Query Match   92.2%; Score 1587; DB 6; Length 339;
  Best Local Similarity   92.3%; Pred. No. 1e-145;
  Matches 313; Conservative   11; Mismatches   15; Indels   0; Gaps   0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||  ||:|||||||||||||||||||| ||||||||:|||||: ||||||||||||||||
Db          1 MNALNAAMTVIGAGSYGTALAITLARNGHHVVLWGHDPKHIATLQHDRCNAAFLPDVPFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||:|||||||||||:|||||||||| ||||||||||||||||||||
Db         61 DTLHLESDLATALAASRDILVVVPSHVFGQVLRQIKPLMRSDARLVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              |||||||||| |||||||||||||||||||||||||||:||  ||:|||:||||||||||
Db        121 QDVAREALGDDIPLAVISGPTFAKELAAGLPTAISLAATDPQFAEDLQRLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||
Db        181 INPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLVEMSRLGAALGADPETF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              ||||||||||||||:|||||||||||||||||||||:|||||||||||||| || |
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQDKIGQVVEGYRNTKEVRVLAQRL 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||||| ||||||||||||||||||:
Db        301 GVEMPITEEIYQVLYCGKIAREAALTLLGRARKDERSSN 339
```

RESULT 12
ABO64223
ID ABO64223 standard; protein; 345 AA.
XX
AC ABO64223;
XX
DT 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polypeptide seqid 10740.
XX
KW Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
OS Klebsiella pneumoniae.
XX
PN US6610836-B1.
XX
PD 26-AUG-2003.
XX
PF 27-JAN-2000; 2000US-00489039.
XX
PR 29-JAN-1999; 99US-0117747P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL, Osborne M;
XX
DR WPI; 2003-895346/82.
DR N-PSDB; ACH97774.
XX

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 10740; 932pp; English.
XX
CC The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention
XX
SQ Sequence 345 AA;

Query Match 92.2%; Score 1587; DB 7; Length 345;
Best Local Similarity 92.3%; Pred. No. 1.1e-145;
Matches 313; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||  ||:||||||||||||||||||||| |||||||:|||||: ||||||||||||||
Db          7 MNALNAAMTVIGAGSYGTALAITLARNGHHVVLWGHDPKHIATLQHDRCNAAFLPDVPFP 66

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||||||||||||||||:||||||||||:|||||||||| ||||||||||||||||||||
Db         67 DTLHLESDLATALAASRDILVVVPSHVFGQVLRQIKPLMRSDARLVWATKGLEAETGRLL 126

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              |||||||||| |||||||||||||||||||||||||:||  ||:|||:||||||||||||
Db        127 QDVAREALGDDIPLAVISGPTFAKELAAGLPTAISLAATDPQFAEDLQRLLHCGKSFRVY 186

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||  ||
Db        187 INPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLVEMSRLGAALGADPETF 246

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:|||||||||||||||||||||:|||||||||||||||| || |
Db        247 MGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQDKIGQVVEGYRNTKEVRVLAQRL 306

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDERSSH 339
              |||||||||||||||| ||||||||||||||||||:
Db        307 GVEMPITEEIYQVLYCGKIAREAALTLLGRARKDERSSN 345
```

RESULT 13
ABU50149
ID ABU50149 standard; protein; 339 AA.
XX
AC ABU50149;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #35676.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Yersinia pestis.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA54019.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 78073; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 339 AA;

Query Match 84.5%; Score 1455; DB 6; Length 339;
Best Local Similarity 84.2%; Pred. No. 7.5e-133;
Matches 283; Conservative 24; Mismatches 29; Indels 0; Gaps 0;

```
Qy          1 MNQRNASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFP 60
              ||   ||| |||||||||||||||||:||||||:||  |::|||| |||||  ||
Db          1 MNTNPASMAVIGAGSYGTALAITLARNGHQVVLWGHDPKHIQQLQQDRCNRAFLPDAAFP 60

Qy         61 DTLHLESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLL 120
              ||| ||:||| ||||||::|||||||||| || |:|| :| |||:||||||||||||||
Db         61 DTLRLETDLACALAASRDVLVVVPSHVFGAVLHQLKPHLRKDARIVWATKGLEAETGRLL 120

Qy        121 QDVAREALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVY 180
              |||||| ||: ||||||||||||||||||||||:|||||  |::|||||||||||||||
Db        121 QDVAREVLGEAIPLAVISGPTFAKELAAGLPTAIALASTDVQFSEDLQQLLHCGKSFRVY 180

Qy        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATF 240
              ||||||||||||||||||||||||||||||||||||||||||:||| ||||||:||
Db        181 SNPDFIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMTRLGTALGADPSTF 240

Qy        241 MGMAGLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRF 300
              |||||||||||||:|||||||:|||||: |: ||: |||||||||||||  || |
Db        241 MGMAGLGDLVLTCTDNQSRNRRFGIMLGQGLGVKEAQDNIGQVVEGYRNTKEVLALAQRH 300

Qy        301 GVEMPITEEIYQVLYCGKNAREAALTLLGRARKDER 336
              ||||||||:||||||| |||||||||||||| :|||:
Db        301 GVEMPITEQIYQVLYCHKNAREAALTLLGRTKKDEK 336
```

RESULT 14
ADF07218
ID ADF07218 standard; protein; 340 AA.
XX
AC ADF07218;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bacterial polypeptide #3331.
XX
KW Proteus mirabilis infection; bacterial infection; antibacterial;
KW immunostimulant.
XX
OS Proteus mirabilis.
XX
PN US6605709-B1.
XX
PD 12-AUG-2003.
XX
PF 05-APR-2000; 2000US-00543681.
XX
PR 09-APR-1999; 99US-0128706P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL;
XX
DR WPI; 2003-895291/82.
DR N-PSDB; ADF03046.
XX
PT New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX
PS Disclosure; SEQ ID NO 7503; 870pp; English.
XX
CC The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX
SQ Sequence 340 AA;

Query Match 82.5%; Score 1420; DB 7; Length 340;
Best Local Similarity 82.3%; Pred. No. 2e-129;
Matches 275; Conservative 28; Mismatches 31; Indels 0; Gaps 0;

```
Qy          5 NASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPDTLH 64
              |||||||||||||||||||||||:||||||||:|:| ||: ||| |||||| |||:|:
Db          5 NASMTVIGAGSYGTALAITLARNGHDVVLWGHDPKHVAALEQARCNQAFLPDVSFPDSLY 64

Qy         65 LESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLLQDVA 124
              :|: |  |: |||||||||:|||||||:|||| :| |||:|||||||| |||||||||
Db         65 MEASLQKAIEASRNILVVIPSHVFGEVLQQIKPFLRQDARVVWATKGLEAHTGRLLQDVA 124

Qy        125 REALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVYSNPD 184
              || ||::|||||:||||||||||||||||::|||| | : |||| ||||||||| |||
Db        125 REVLGNEIPLAVLSGPTFAKELAAGLPTAIAVASTDNLFLEQLQQLFHCGKSFRVYKNPD 184

Qy        185 FIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATFMGMA 244
              ||||||||||||||||||||:||||||||||||||||||| ||||| |||||||
Db        185 FIGVQLGGAVKNVIAIGAGMSDGMGFGANARTALITRGLAEMSRLGKALGADAATFMGMA 244

Qy        245 GLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEM 304
              ||||||||||:|||||||||||||||||:|| :|||||||||||||||||| || : ||||
Db        245 GLGDLVLTCTDNQSRNRRFGMMLGQGLDVDTAQEKIGQVVEGYRNTKEVRALAEQVGVEM 304

Qy        305 PITEEIYQVLYCGKNAREAALTLLGRARKDERSS 338
              ||||:|||:||  |: :|||| ||||| |||  |
Db        305 PITEQIYQILYQHKDVKEAALALLGRATKDEIDS 338
```

RESULT 15
ABU40593
ID ABU40593 standard; protein; 337 AA.
XX
AC ABU40593;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #26120.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Proteus sp.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA44463.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 68517; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational

```
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC   the target prokaryotic essential genes. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 337 AA;

  Query Match             81.9%;  Score 1411;  DB 6;  Length 337;
  Best Local Similarity   82.0%;  Pred. No. 1.5e-128;
  Matches  274;  Conservative   27;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          5 NASMTVIGAGSYGTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFPDTLH 64
              |||||||||||||||||||||||:||||||||:|:| ||: ||| |||||| |||:|:
Db          2 NASMTVIGAGSYGTALAITLARNGHDVVLWGHDPKHVAALEQARCNQAFLPDVSFPDSLY 61

Qy         65 LESDLATALAASRNILVVVPSHVFGEVLRQIKPLMRPDARLVWATKGLEAETGRLLQDVA 124
              :|: |   |: |||||||:||||||||:|||| :| |||:|||||||| |||||||||
Db         62 MEASLQKAIEASRNILVVIPSHVFGEVLQQIKPFLRQDARVVWATKGLEAHTGRLLQDVA 121

Qy        125 REALGDQIPLAVISGPTFAKELAAGLPTAISLASTDQTFADDLQQLLHCGKSFRVYSNPD 184
              || ||::|||||:|||||||||||||||::||||   | : |||| ||||||||| |||
Db        122 REVLGNEIPLAVLSGPTFAKELAAGLPTAIAVASTDNLFLEQLQQLFHCGKSFRVYKNPD 181

Qy        185 FIGVQLGGAVKNVIAIGAGMSDGIGFGANARTALITRGLAEMSRLGAALGADPATFMGMA 244
              |||||||||||||||||||:|||||||||||||||||||||| ||||| |||||||
Db        182 FIGVQLGGAVKNVIAIGAGMSDGMGFGANARTALITRGLAEMSRLGKALGADAATFMGMA 241

Qy        245 GLGDLVLTCTENQSRNRRFGMMLGQGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEM 304
              ||||||||||:|||||||||||||   | :|||||||||||||||| || : ||||
Db        242 GLGDLVLTCTDNQSRNRRFGMMLGQGFGVDTAQEKIGQVVEGYRNTKEVRALAEQVGVEM 301

Qy        305 PITEEIYQVLYCGKNAREAALTLLGRARKDERSS 338
              ||||:|||:||   |: :|||| ||||| |||   |
Db        302 PITEQIYQILYQHKDVKEAALALLGRATKDEIDS 335


Search completed: April 27, 2005, 10:59:44
Job time : 167 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 27, 2005, 09:52:56 ; Search time 656 Seconds
(without alignments)
9204.476 Million cell updates/sec

Title: US-10-088-079-1
Perfect score: 1020
Sequence: 1 atgaaccaacgtaatgcttc.....acgagcgcagcagccactaa 1020

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1020	100.0	1020	5	AAF57428	Aaf57428 E. coli g
2		1018.4	99.8	1020	4	AAS52655	Aas52655 E. coli D
3		1018.4	99.8	1020	8	ACA32689	Aca32689 Prokaryot
4		1018.4	99.8	1020	13	ADT48853	Adt48853 Bacterial
5		787	77.2	1020	8	ACA51335	Aca51335 Prokaryot
6		765.8	75.1	1017	8	ACA31966	Aca31966 Prokaryot
7		756.8	74.2	1017	8	ACA35838	Aca35838 Prokaryot
8		756.6	74.2	1038	11	ACH97774	Ach97774 Klebsiell
9		749.4	73.5	1023	8	ACA49224	Aca49224 Prokaryot
10		606	59.4	1020	8	ACA54019	Aca54019 Prokaryot
11	c	565.6	55.5	781	6	ABQ21987	Abq21987 Oligonucl
12		565.6	55.5	781	6	ABQ21986	Abq21986 Oligonucl
13		556.4	54.5	1023	10	ACF70491	Acf70491 Photorhab
14		556.4	54.5	69727	10	ACF65374	Acf65374 Photorhab
15		556.4	54.5	110000	10	ACF67367_35	Continuation (36 o
16		539.6	52.9	1011	8	ACA44463	Aca44463 Prokaryot
17		539.6	52.9	1023	10	ADF03046	Adf03046 Bacterial
18		539.4	52.9	990	13	ADS45613	Ads45613 Bacterial
19		521.2	51.1	990	13	ADT46572	Adt46572 Bacterial
20		513.8	50.4	781	6	ABQ21989	Abq21989 Oligonucl
21	c	513.8	50.4	781	6	ABQ21988	Abq21988 Oligonucl
22		476.2	46.7	1035	8	ACA53490	Aca53490 Prokaryot
23		414.4	40.6	1014	8	ACA43241	Aca43241 Prokaryot
24		399.4	39.2	135356	13	ADT05646	Adt05646 Haemophil
25		396.2	38.8	1008	4	AAS53331	Aas53331 Haemophil
26		396.2	38.8	1008	8	ACA34182	Aca34182 Prokaryot
27		396.2	38.8	110000	2	AAT42063_06	Continuation (7 of
28	c	388.4	38.1	4711	13	ADT05428	Adt05428 Haemophil
29		325.6	31.9	503	6	ABQ50341	Abq50341 Oligonucl
30	c	325.6	31.9	503	6	ABQ50340	Abq50340 Oligonucl
31	c	313.8	30.8	503	6	ABQ50339	Abq50339 Oligonucl
32		313.8	30.8	503	6	ABQ50338	Abq50338 Oligonucl
33		238.6	23.4	1002	13	ADT41591	Adt41591 Bacterial
34		238.6	23.4	1002	13	ADS63997	Ads63997 Bacterial
35		238.6	23.4	1020	13	ADS63622	Ads63622 Bacterial
36		221	21.7	1041	13	ADT42864	Adt42864 Bacterial
37		219.4	21.5	987	8	ACA37060	Aca37060 Prokaryot
38		211.4	20.7	1002	13	ADS57169	Ads57169 Bacterial
39		199.8	19.6	987	8	ABX09916	Abx09916 N. mening
40		199.8	19.6	49767	3	AAA81458	Aaa81458 N. mening
41	c	199.8	19.6	110000	3	AAA81489_7	Continuation (8 of
42	c	199.8	19.6	110000	4	AAI99682_33	Continuation (34 o
43	c	199.8	19.6	110000	4	AAI99683_33	Continuation (34 o
44	c	199.8	19.6	172325	3	AAF21613	Aaf21613 Neisseria
45		199.6	19.6	1002	8	ACA38486	Aca38486 Prokaryot

ALIGNMENTS

RESULT 1
AAF57428
ID AAF57428 standard; DNA; 1020 BP.
XX
AC AAF57428;
XX
DT 11-JUN-2001 (first entry)
XX
DE E. coli gpsA2FR encoding DNA.
XX
KW Glycerol-3-phosphate dehydrogenase; G3PD; feedback inhibition; oil seed;
KW genetic transformation; fatty acid; glycerolipid; osmotic stress; gpsA;
KW gpsA2FR; allele; ds.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
FT CDS 1. .1020
FT /*tag= a
FT /product= "gpsA2FR"
FT mutation 765
FT /*tag= b
FT /note= "there is a point mutation at this position as
FT compared to the wild-type gpsA gene, which makes the gene
FT feed-defective; wild-type GAC codon is changed to GAA
FT codon"
XX
PN WO200121820-A1.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-CA001096.
XX
PR 22-SEP-1999; 99US-0155133P.
XX
PA (CANA) NAT RES COUNCIL CANADA.
XX
PI Zou J, Wei Y, Periappuram C, Selvaraj G, Datla R;
XX
DR WPI; 2001-257996/26.
DR P-PSDB; AAB62189.
XX
PT Manipulating glycerol-3-phosphate metabolism of plant for enhancing

PT stress tolerance, altering fatty acid content in glycerolipids, by
PT expressing in plant feedback defective glycerol-3-phosphate dehydrogenase
PT gene.
XX
PS Claim 5; Fig 1; 39pp; English.
XX
CC The invention provides a method for genetically transforming a plant so
CC that it expresses a a heterologous glycerol-3-phosphate dehydrogenase
CC (G3PD) that is less sensitive to feedback inhibition than wild-type G3PD.
CC The method involves providing a vector comprising a DNA sequence encoding
CC G3PD that is less sensitive to feedback inhibition than wild-type G3PD
CC and transforming the plant with the vector. The method is useful for
CC expressing a heterologous G3PD less sensitive to feedback inhibition than
CC wild-type G3PD in an oil seed bearing plant, such as Arabidopsis thaliana
CC or Brassica. The vectors are useful for producing a genetically altered
CC plant having altered fatty acid content in its glycerolipids, especially
CC elevated levels of C16 fatty acids and increased osmotic stress tolerance
CC relative to the wild type. The present sequence represents the DNA
CC encoding the E. coli gpsA2FR protein. The gene gpsA2FR is an allele of
CC the E. coli gpsA gene, and encodes an altered version of the GPDH protein
CC defective in feedback inhibition. This gpsA2FR gene can be used in the
CC vectors and method of the invention
XX
SQ Sequence 1020 BP; 214 A; 274 C; 304 G; 228 T; 0 U; 0 Other;

Query Match 100.0%; Score 1020; DB 5; Length 1020;
Best Local Similarity 100.0%; Pred. No. 2.1e-308;
Matches 1020; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60

Qy         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120

Qy        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180

Qy        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240

Qy        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300

Qy        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360

Qy        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420

Qy        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480

Qy        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540

Qy        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600

Qy        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660

Qy        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720

Qy        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780

Qy        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840

Qy        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900

Qy        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960

Qy        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTAA 1020
```

RESULT 2
AAS52655
ID AAS52655 standard; DNA; 1020 BP.
XX
AC AAS52655;
XX
DT 13-FEB-2002 (first entry)
XX
DE E. coli DNA for cellular proliferation protein #377.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
KW antibacterial; drug design.
XX
OS Escherichia coli.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU34796.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Claim 27; SEQ ID NO 6292; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

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CC   useful for the identification of potential new targets for antibiotic
CC   development. The antisense nucleic acids can also be used to identify
CC   proteins used in proliferation, to express these proteins, and to obtain
CC   antibodies capable of binding to the expressed proteins. The proteins can
CC   be used to screen compounds in rational drug discovery programmes. The
CC   antisense nucleic acid sequence is also useful to screen for homologous
CC   nucleic acids which are required for cell proliferation in a wide variety
CC   of organisms. The present sequence encodes an essential prokaryotic
CC   cellular proliferation protein. Note: The sequence data for this patent
CC   did not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 1018.4;  DB 4;  Length 1020;
  Best Local Similarity   99.9%;  Pred. No. 6.8e-308;
  Matches 1019;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60

Qy         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120

Qy        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180

Qy        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240

Qy        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300

Qy        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360

Qy        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420

Qy        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480

Qy        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540

Qy        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600

Qy        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660

Qy        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720

Qy        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGACAACCAGTCGCGTAAC 780

Qy        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840

Qy        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900

Qy        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960

Qy        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTAA 1020


RESULT 3
ACA32689
ID   ACA32689 standard; DNA; 1020 BP.
XX
AC   ACA32689;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #14346.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Escherichia coli.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU28819.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 20559; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
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CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 1018.4;  DB 8;  Length 1020;
  Best Local Similarity   99.9%;  Pred. No. 6.8e-308;
  Matches 1019;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60

Qy         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120

Qy        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180

Qy        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240

Qy        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300

Qy        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360

Qy        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420

Qy        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480

Qy        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540

Qy        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600

Qy        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660

Qy        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720

Qy        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGACAACCAGTCGCGTAAC 780

Qy        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840

Qy        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900

Qy        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960

Qy        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTAA 1020


RESULT 4
ADT48853
ID   ADT48853 standard; cDNA; 1020 BP.
XX
AC   ADT48853;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Bacterial polynucleotide #23604.
XX
KW   Recombinant DNA construct; transformed plant; improved plant property;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW   pathogen tolerance; pest tolerance; plant disease resistance;
KW   cell cycle pathway modification; plant growth regulator;
KW   homologous recombination; seed oil yield; protein yield; carbohydrate;
KW   nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW   bacterial polynucleotide; gene; ss.
XX
OS   Bacteria.
XX
PN   US2003233675-A1.
XX
PD   18-DEC-2003.
XX
PF   20-FEB-2003; 2003US-00369493.
XX
PR   21-FEB-2002; 2002US-0360039P.
XX
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
XX
PI   Cao Y,  Hinkle GJ,  Slater SC,  Chen X,  Goldman BS;
XX
DR   WPI; 2004-061375/06.
XX
PT   New recombinant DNA construct comprising a promoter positioned to provide
PT   for expression of a polynucleotide encoding a polypeptide from a
PT   microbial source, useful for producing plants with improved properties.
XX
PS   Claim 1; SEQ ID NO 47291; 122pp; English.
XX
CC   The invention relates to a recombinant DNA construct comprising a
CC   promoter functional in a plant cell, where the promoter is positioned to
CC   provide for expression of a polynucleotide encoding a polypeptide from a
CC   microbial source. The invention also relates to a transformed plant
CC   comprising the recombinant DNA construct and a method of producing a
CC   transformed plant having an improved property. The plant is a crop plant
CC   such as maize or soybean. The method of producing a transformed plant
CC   having an improved property comprises transforming a plant with the
CC   recombinant DNA construct and growing the transformed plant, where the
CC   polynucleotide or polypeptide is useful for improving plant properties.
CC   The recombinant DNA construct is useful for producing plants with
CC   improved plant properties, e.g. improved cold, heat or drought tolerance,
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CC   tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC   increased resistance to plant disease, better growth rate by modification
CC   of the cell cycle pathway with plant growth regulators, increased rate of
CC   homologous recombination, modified seed oil or protein yield and/or
CC   content, improved yield by modification of carbohydrate, nitrogen or
CC   phosphorus use and/or uptake, by modification of photosynthesis or by
CC   providing improved plant growth and development under at least one stress
CC   condition, improved lignin production or improved galactomannan
CC   production. This sequence represents a bacterial polynucleotide used in
CC   the scope of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification but was obtained in electronic
CC   format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 1020 BP; 213 A; 275 C; 304 G; 228 T; 0 U; 0 Other;

  Query Match            99.8%;  Score 1018.4;  DB 13;  Length 1020;
  Best Local Similarity  99.9%;  Pred. No. 6.8e-308;
  Matches 1019;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60

Qy         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120

Qy        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180

Qy        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240

Qy        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300

Qy        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360

Qy        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420

Qy        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480

Qy        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540

Qy        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600

Qy        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660

Qy        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720

Qy        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGACAACCAGTCGCGTAAC 780

Qy        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840

Qy        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900

Qy        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960

Qy        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTAA 1020


RESULT 5
ACA51335
ID   ACA51335 standard; DNA; 1020 BP.
XX
AC   ACA51335;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #32992.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Salmomella typhi.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU47465.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 39205; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
```

```
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1020 BP; 217 A; 271 C; 316 G; 216 T; 0 U; 0 Other;

  Query Match             77.2%;  Score 787;  DB 8;  Length 1020;
  Best Local Similarity   85.8%;  Pred. No. 2e-235;
  Matches  874;  Conservative    0;  Mismatches  145;  Indels    0;  Gaps    0;

Qy          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
              ||||||||| ||||||| |||||||| || ||||||||||||||||||||||||||||||
Db          1 ATGAACCAAAGTAATGCGTCAATGACAGTCATCGGTGCCGGCTCGTACGGCACCGCTCTC 60

Qy         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120
              |||||||| ||||| ||||| |||||| |||||||||| |||||||| |||||  |||||
Db         61 GCCATCACTCTGGCGAGAAACGGCCACCAGGTTGTCCTGTGGGGCCACGACCCAAAACAT 120

Qy        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180
              ||||| || || || | ||| ||||| |||| |||||| || ||||||||||||||||||
Db        121 ATCGCGACCCTGGAGCACGATCGCTGCAACGTCGCGTTCCTTCCCGATGTGCCTTTTCCC 180

Qy        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240
              |||||| | || || |||||||| | || || |||||||| ||||| ||||| |||||
Db        181 GATACGTTACACCTGGAAAGCGACTTAGCAACCGCGCTGGCGGCCAGTCGTAACATTCTG 240

Qy        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300
              || || || || |||||||| ||  | || |||||||| |||||||||| |||||||||
Db        241 GTGGTGGTGCCAAGCCATGTTTTCAGCGACGTGCTGCGGCAGATTAAACCGCTGATGCGT 300

Qy        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360
              || |||||||||||||| |||||||||||||| |||||||||||||| || || |||||
Db        301 CCGGATGCGCGTCTGGTATGGGCGACCAAAGGCCTGGAAGCGGAAACGGGGCGCCTGTTG 360

Qy        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420
              ||||| || || || ||||| |||||||||||||| |||||||||| || || || ||
Db        361 CAGGATGTCGCTCGCGAGGCGTTAGGCGATCAAATCCCGCTGGCGGTGATTTCCGGTCCG 420

Qy        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
              ||||| || ||||| |||||||| ||||| ||||| || || ||||| ||||| ||||||
Db        421 ACGTTCGCTAAAGAGCTGGCGGCGGGTTTGCCGACGGCAATCTCGCTAGCCTCAACCGAT 480

Qy        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540
              |||||||||||||| |||||||||| ||| |||||||||| |||||||| ||||| ||
Db        481 GAGACCTTTGCCGACGATCTCCAGCAACTGTTGCACTGCGGAAAAAGTTTTCGCGTCTAT 540

Qy        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600
              | |||| ||||||| || |||||||||||||||||||||||||||||| ||||| |||
Db        541 ATCAATGCGGATTTTATCGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTGATTGCGATT 600

Qy        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660
              || |||||||||| |||| ||||| || || ||||| || || |||||||| ||||| 
Db        601 GGCGCGGGGATGTCTGACGGCATCGGCTTCGGCGCGAACGCCCGCACGGCGCTAATCACG 660

Qy        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720
              ||||| ||| | |||||||||| ||||| || ||||| |||||||| || |||||||||
Db        661 CGTGGACTGACCGAAATGTCGCGGCTTGGCGCAGCGCTTGGTGCCGATCCCGCCACCTTT 720

Qy        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780
              ||||| |||||||| | |||||||||||||| |||||||||| |||||||||| |||
Db        721 ATGGGGATGGCGGGTTTAGGCGATCTGGTGCTGACCTGTACCGACAACCAGTCGCGCAAC 780

Qy        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840
              || |||||||||||||||| || |||||||||| ||  || |||||||||| ||||||
Db        781 CGTCGTTTTGGCATGATGCTTGGCCAGGGCATGGACGTTAAAGGCGCGCAGGATAAGATT 840

Qy        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900
              || |||||||| |||||||| |||||||||||||||||| || ||| |||||||| || ||
Db        841 GGCCAGGTGGTCGAAGGCTATCGCAATACGAAAGAAGTTCGTGAATTGGCGCACCGTTTT 900

Qy        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960
              || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        901 GGTGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTGTATTGCGGAAAAAACGCG 960

Qy        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTA 1019
              |||||||||||||| || ||| ||||||| || |||||||| |||| || |||||||
Db        961 CGCGAGGCAGCATTAACGTTATTAGGTCGCGCCCGCAAGGAAGAGCTGAGTCGCCACTA 1019


RESULT 6
ACA31966
ID   ACA31966 standard; DNA; 1017 BP.
XX
AC   ACA31966;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #13623.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Enterobacter cloacae.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU28096.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 19836; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
```

CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1017 BP; 207 A; 289 C; 312 G; 209 T; 0 U; 0 Other;

Query Match 75.1%; Score 765.8; DB 8; Length 1017;
Best Local Similarity 84.6%; Pred. No. 8.6e-229;
Matches 860; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

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Qy          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
              ||||  |     ||||||||||||||||||||||||||||| ||||||||||||||||
Db          1 ATGAGCACTGTTAATGCGTCAATGACTGTGATCGGTGCCGGCTCATACGGCACCGCTCTT 60

Qy         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120
              |||||||| |||||||||||||| ||||| || || |||||||||| |||||  |||||
Db         61 GCCATCACGCTGGCAAGAAATGGTCACGAAGTGGTTCTCTGGGGCCACGACCCAAAACAT 120

Qy        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180
              ||||||||||  |||||||||| |||||||  |||||||| || || ||.|| || |||
Db        121 ATCGCAACGCTGCAACGCGACCGTTGTAACGTGGCGTTTCTTCCGGACGTTCCGTTCCCC 180

Qy        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240
              ||  | || || |||||||||| || || || |||||||| |||||||| || |||||
Db        181 GACTCCCTGCACCTTGAAAGCGACCTTGCGACCGCGCTGGCGGCCAGCCGCAACATTCTG 240

Qy        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300
              | || || || |||||||| ||||| || ||||| || |||||||| || |||||||||
Db        241 ATTGTGGTTCCGAGCCATGTATTTGGCGACGTGCTCCGTCAGATTAAGCCGCTGATGCGC 300

Qy        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360
              || ||||||||  | || |||||||| ||||| |||||||| |||||||||| ||| |
Db        301 CCGGATGCGCGCATTGTCTGGGCGACAAAAGGACTGGAAGCCGAAACCGGACGCCTGCTG 360

Qy        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420
              |||||||| || || || ||  | || |||  || |||||||||| ||||| |||||
Db        361 CAGGACGTTGCCCGCGAAGCGCTGGGTGATGCGATCCCGCTGGCGGTCATCTCCGGCCCG 420

Qy        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
              || ||||| ||||| ||||| || ||  | ||||| || |||||||||||||| ||||||
Db        421 ACCTTTGCCAAAGAGCTGGCCGCTGGCCTGCCGACGGCGATTTCGCTGGCCTCCACCGAT 480

Qy        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540
              |||  ||||  |||| ||||| || |||||||||||||||||| || |||||||| |||
Db        481 CAGGCCTTCTCCGACGATCTTCAACAGCTGCTGCACTGCGGCAAGAGCTTCCGCGTCTAC 540

Qy        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600
              ||||| || ||||| || |||||||| || ||||| |||||||| ||||| ||||| |||
Db        541 AGCAACCCCGATTTTATCGGCGTGCAACTGGGCGGTGCGGTGAAGAACGTGATTGCGATT 600

Qy        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660
              || || |||||||| ||||| || |||||||||| |||||||||||||||||||||||||
Db        601 GGCGCCGGGATGTCAGACGGCATTGGTTTTGGTGCCAATGCGCGTACGGCGCTGATCACC 660

Qy        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720
              || |||||  | |||||||| || || || |  |||||||||||||| || |||||||||
Db        661 CGAGGGCTAACCGAAATGTCCCGCCTGGGCGAAGCGCTGGGTGCCGATCCGGCCACCTTT 720

Qy        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780
              ||||| ||||| || || ||||| |||||||| |||||||||| |||||||| ||||||
Db        721 ATGGGAATGGCTGGCCTGGGCGACCTGGTGCTGACCTGTACCGATAACCAGTCTCGTAAC 780

Qy        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840
              |||||||||||||||||||||||| |||||||  |||||  || ||||||||||||||||
Db        781 CGCCGTTTTGGCATGATGCTCGGACAGGGCAGCGATGTTAAAGGCGCGCAGGAGAAGATT 840

Qy        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900
              |||||||||| |||||||||||||||| |||||||||||||  ||||||| || |||
Db        841 GGTCAGGTGGTTGAAGGCTACCGCAATACCAAAGAAGTCCGCGAGTTGGCGCACCGTTTC 900

Qy        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960
              || || |||||||||||||||||||||||||||| ||||| |||||||||||||  |||
Db        901 GGTGTCGAAATGCCAATAACCGAGGAAATTTATCAGGTATTGTATTGCGGAAAAAATGCG 960

Qy        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCAC 1017
              |||||||||||||||| ||| |||||||||| ||||||||||||||||||||  ||
Db        961 CGCGAGGCAGCATTGACCTTATTAGGTCGTGCGCGCAAGGACGAGCGCAGCAGTAAC 1017
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RESULT 7
ACA35838
ID ACA35838 standard; DNA; 1017 BP.
XX
AC ACA35838;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #17495.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Klebsiella pneumoniae.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU31968.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 23708; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)

```
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1017 BP; 194 A; 306 C; 319 G; 198 T; 0 U; 0 Other;

  Query Match             74.2%;  Score 756.8;  DB 8;  Length 1017;
  Best Local Similarity   84.1%;  Pred. No. 5.7e-226;
  Matches  854;  Conservative    0;  Mismatches  162;  Indels    0;  Gaps    0;

Qy          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
              ||||||  || ||||||| ||||||||||||||||||||||| ||||||||||||||||
Db          1 ATGAACGCACTTAATGCTGCAATGACTGTGATCGGTGCCGGCTCTTACGGCACCGCTCTT 60

Qy         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120
              |||||||||||||||||||||||| | ||||| || ||||||||||||||  |||||
Db         61 GCCATCACCCTGGCAAGAAATGGCCACCACGTTGTGCTGTGGGGCCATGACCCGAAACAT 120

Qy        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180
              ||||| |||||  ||| ||| ||||| |||||||||| || ||||||||||||||| ||
Db        121 ATCGCGACGCTGCAACACGATCGCTGCAACGCCGCGTTCCTTCCCGATGTGCCTTTCCCG 180

Qy        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240
              |||||||| |||||||| ||||| || ||||| |||||||| ||||||||  | || ||
Db        181 GATACGCTGCATCTTGAGAGCGACCTGGCCACCGCGCTGGCCGCCAGCCGCGACATCCTT 240

Qy        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300
              ||||| || || |||||||| || ||| | ||| | |||||||||||||| |||||||||
Db        241 GTCGTGGTGCCGAGCCATGTATTCGGTCAGGTGTTACGCCAGATTAAACCGCTGATGCGT 300

Qy        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360
              | || ||||| |||||||||| |||||||| || || || |||||||| |||||| |
Db        301 TCCGACGCGCGGCTGGTGTGGGCCACCAAAGGCCTTGAGGCCGAAACCGGCCGTCTGCTG 360

Qy        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420
              |||||||||||||||| ||   | |||||| | |||||||||||| ||||| || |||
Db        361 CAGGACGTGGCGCGTGAAGCGCTGGGCGATGATATTCCGCTGGCGGTGATCTCGGGGCCA 420

Qy        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
              || || || ||||| ||||| || ||  | ||||| || ||||||||||  | || |||
Db        421 ACCTTCGCCAAAGAGCTGGCCGCCGGCCTGCCGACGGCGATTTCGCTGGCGGCCACGGAT 480

Qy        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540
              | |   ||||| || || || ||||  || |||||||||||||||| |||||||| |||
Db        481 CCGCAGTTTGCGGAGGACCTTCAGCGCCTACTGCACTGCGGCAAAAGCTTCCGCGTCTAC 540

Qy        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600
              | ||| ||||| || || |||||||||| |||||||||||||||||||| ||||||||
Db        541 ATCAACCCGGACTTTATCGGCGTGCAGCTCGGCGGCGCGGTGAAAAACGTCATTGCCATC 600

Qy        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660
              || || ||||| ||||| ||||| || || || |||||||||||||||||||| |||
Db        601 GGGGCAGGTATGTCGGACGGCATCGGCTTCGGCGCCAATGCGCGTACGGCGCTGATTACC 660

Qy        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720
              |||||||||  |||||||| || || || |||||||||| ||||| || |  ||||||
Db        661 CGTGGGCTGGTGGAAATGTCCCGCCTCGGCGCGGCGCTGGGCGCCGATCCGGAAACCTTT 720

Qy        721 ATGGGCATGGCGGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780
              |||||||||| || || || || |||||||| ||||| ||||| |||||||| ||||||
Db        721 ATGGGCATGGCCGGCCTCGGTGACCTGGTGCTCACCTGCACCGACAACCAGTCCCGTAAC 780

Qy        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840
              || || || |||||||||||||| ||||| ||||| || || ||||| ||||| ||||||
Db        781 CGTCGCTTCGGCATGATGCTCGGCCAGGGTATGGACGTGCAGAGCGCCCAGGACAAGATT 840

Qy        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900
              || |||||||| |||||||||||||||| || ||||| |||| |||||| || || ||
Db        841 GGCCAGGTGGTTGAAGGCTACCGCAATACCAAGGAAGTTCGCGTTCTGGCACAGCGTTTA 900

Qy        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960
              || || ||||||||||||||||||||||||||| ||||| |||||||||||||   |||
Db        901 GGTGTCGAAATGCCAATAACCGAGGAAATTTATCAGGTATTGTATTGCGGAAAAATTGCG 960

Qy        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCA 1016
              |||||||||||||||| ||| | ||||| || ||||||||||||||||||||| |
Db        961 CGCGAGGCAGCATTGACCTTATTGGGTCGCGCCCGCAAGGACGAGCGCAGCAGCAA 1016


RESULT 8
ACH97774
ID   ACH97774 standard; DNA; 1038 BP.
XX
AC   ACH97774;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Klebsiella pneumoniae polynucleotide seqid 3569.
XX
KW   Recombinant expression vector; transcription regulatory element;
KW   Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.
XX
OS   Klebsiella pneumoniae.
XX
PN   US6610836-B1.
XX
PD   26-AUG-2003.
XX
PF   27-JAN-2000; 2000US-00489039.
XX
PR   29-JAN-1999;   99US-0117747P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Breton GL,  Osborne M;
XX
DR   WPI; 2003-895346/82.
DR   P-PSDB; ABO64223.
XX
PT   New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT   preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS   Disclosure; SEQ ID NO 3569; 932pp; English.
XX
CC   The invention describes a new isolated nucleic acid encoding a Klebsiella
CC   pneumoniae polypeptide. Also described are: a recombinant expression
CC   vector comprising the nucleic acid, operably linked to a transcription
CC   regulatory element; and a cell comprising the recombinant expression
CC   vector. The nucleic acid is useful for preparing a vaccine composition
CC   against Klebsiella pneumoniae. This sequence encodes a Klebsiella
CC   pneumoniae polypeptide of the invention
XX
SQ   Sequence 1038 BP; 201 A; 310 C; 324 G; 203 T; 0 U; 0 Other;

  Query Match             74.2%;  Score 756.6;  DB 11;  Length 1038;
  Best Local Similarity   83.9%;  Pred. No. 6.6e-226;
  Matches  855;  Conservative    0;  Mismatches  164;  Indels    0;  Gaps    0;

Qy          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
              ||||||  || ||||||| ||||||||||||||||||||||| ||||||||||||||||
Db         19 ATGAACGCACTTAATGCTGCAATGACTGTGATCGGTGCCGGCTCTTACGGCACCGCTCTT 78
```

```
Qy        61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120
             |||||||||||||||||||||||||| | ||||| || ||||||||||||||  |||||
Db        79 GCCATCACCCTGGCAAGAAATGGCCACCACGTTGTGCTGTGGGGCCATGACCCGAAACAT 138

Qy       121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180
             ||||| |||||  ||| ||| |||||| |||||||||| || ||||||||||||||| ||
Db       139 ATCGCGACGCTGCAACACGATCGCTGCAACGCCGCGTTCCTTCCCGATGTGCCTTTCCCG 198

Qy       181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240
             |||||||| |||||||| ||||| || ||||| |||||||| ||||||||  | || ||
Db       199 GATACGCTGCATCTTGAGAGCGACCTGGCCACCGCGCTGGCCGCCAGCCGCGACATCCTT 258

Qy       241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300
             ||||||  || || |||||||| || ||| | ||| | |||||||||||||| |||||||||
Db       259 GTCGTGGTGCCGAGCCATGTATTCGGTCAGGTGTTACGCCAGATTAAACCGCTGATGCGT 318

Qy       301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360
               | || ||||| |||||||||| |||||||| || || || |||||||| |||||| |
Db       319 TCCGACGCGCGGCTGGTGTGGGCCACCAAAGGCCTTGAGGCCGAAACCGGCCGTCTGCTG 378

Qy       361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420
             |||||||||||||||| ||   | |||||| | |||||||||||||| ||||| || |||
Db       379 CAGGACGTGGCGCGTGAAGCGCTGGGCGATGATATTCCGCTGGCGGTGATCTCGGGGCCA 438

Qy       421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
             || || || ||||| ||||| || ||   | ||||| || |||||||||||   | || |||
Db       439 ACCTTCGCCAAAGAGCTGGCCGCCGGCCTGCCGACGGCGATTTCGCTGGCGGCCACGGAT 498

Qy       481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540
             | |   ||||| || || || |||| || |||||||||||||||| ||||||| |||
Db       499 CCGCAGTTTGCGGAGGACCTTCAGCGCCTACTGCACTGCGGCAAAAGCTTCCGCGTCTAC 558

Qy       541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600
             | ||| ||||| || || |||||||||| |||||||||||||||||||| ||||||||
Db       559 ATCAACCCGGACTTTATCGGCGTGCAGCTCGGCGGCGCGGTGAAAAACGTCATTGCCATC 618

Qy       601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660
             || || || ||||| || || ||||| || || || |||||||||||||||||| |||
Db       619 GGGGCAGGTATGTCGGATGGCATCGGCTTCGGCGCCAATGCGCGTACGGCGCTGATTACC 678

Qy       661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720
             |||||||||  |||||||| || || || |||||||||| |||| || |  ||||||
Db       679 CGTGGGCTGGTGGAAATGTCCCGCCTCGGCGCGGCGCTGGGCGCCGATCCGGAAACCTTT 738

Qy       721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780
             |||||||||| || || || || |||||||| ||||| ||||| |||||||| ||||||
Db       739 ATGGGCATGGCCGGCCTCGGTGACCTGGTGCTCACCTGCACCGACAACCAGTCCCGTAAC 798

Qy       781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840
             || || || |||||||||||||| ||||| ||||| || || ||||| ||||| ||||||
Db       799 CGTCGCTTCGGCATGATGCTCGGCCAGGGTATGGACGTGCAGAGCGCCCAGGACAAGATT 858

Qy       841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900
             || ||||||| |||||||||||||||| || ||||| |||| |||||  || || ||
Db       859 GGCCAGGTGGTTGAAGGCTACCGCAATACCAAGGAAGTTCGCGTTCTGGCACAGCGTTTA 918

Qy       901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960
             || || |||||||||||||||||||||||| ||||| |||||||||||   |||
Db       919 GGTGTCGAAATGCCAATAACCGAGGAAATTTATCAGGTATTGTATTGCGGAAAAATTGCG 978

Qy       961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTA 1019
             |||||||||||||||| ||| | ||||| || |||||||||||||||||||| | ||
Db       979 CGCGAGGCAGCATTGACCTTATTGGGTCGCGCCCGCAAGGACGAGCGCAGCAGCAATTA 1037
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RESULT 9
ACA49224
ID ACA49224 standard; DNA; 1023 BP.
XX
AC ACA49224;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #30881.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Salmonella paratyphi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU45354.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 37094; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1023 BP; 219 A; 272 C; 313 G; 219 T; 0 U; 0 Other;

Query Match 73.5%; Score 749.4; DB 8; Length 1023;
Best Local Similarity 85.4%; Pred. No. 1.2e-223;
Matches 870; Conservative 0; Mismatches 146; Indels 3; Gaps 3;

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Qy         1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
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Db          1 ATGAACCAAAGTAATGCGTCAATGACAGTCATCGGTGCCGGCTCGTACGGCACC-CTCTC 59

Qy         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120

Db         60 GCCATCACTCTGGCGAGAAACGGCCACCAGGTTGTCCTGTGGGGCCACGACCCAAAACAT 119

Qy        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180

Db        120 ATCGCGACCCTGGAGCACGATCGCTGCAACGTCGCGTTCCTTCCCGATGTGCCTTTTCCC 179

Qy        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240

Db        180 GATACGTTACACCTGGAAAGCGACTTAGCAACCGCGCTGGCGGCCAGTCGTAACATTCTG 239

Qy        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300

Db        240 GTGGTGGTGCCAAGCCATGTTTTCAGCGACGTGCTGCGGCAGATTAAACCGCTGATGCGT 299

Qy        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360

Db        300 CCGGATGCGCGTCTGGTATGGGCGACCAAAGGCCTGGAAGCGGAAACGGGGCGCCTGTTG 359

Qy        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420

Db        360 CAGGATGTCGCTCGCGAAGCGTTAGGCGATCAAATCCCGCTGGCGGTGATTTCTGGCCCG 419

Qy        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480

Db        420 ACGTTCGCTAAAGAATTGGCGGCGGGTTT-GCGACGGCAATCTCTCTGGCCTCAACCGAT 478

Qy        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540

Db        479 GAGACCTTTGCCGACGATCTCCAGCAACTGTTGCACTGCGGAAAAAGTTTTCGCGTCTAT 538

Qy        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600

Db        539 ATCAATGCGGATTTTATCGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTGATTGCGATT 598

Qy        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660

Db        599 GGCGCGGGGATGTCTGACGGCATCGGCTTCGGCGCGAACGCCCGCACGGCGCTAATCACG 658

Qy        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720

Db        659 CGTGGACTGACCGAAATGTCGCGGCTTGGCGC-ACGCTTGGCGCCGATCCCGCCACCTTT 717

Qy        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780

Db        718 ATGGGGATGGCGGGTTTAGGCGATCTGGTGCTGACCTGTACCGACAACCAGTCGCGCAAC 777

Qy        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840

Db        778 CGTCGTTTTGGCATGATGCTTGGCCAGGGCATGGACGTTAAAGGCGCGCAGGATAAGATT 837

Qy        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900

Db        838 GGCCAGGTGGTCGAAGGCTATCGCAATACGAAAGAAGTTCGTGAATTGGCGCACCGTTTT 897

Qy        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960

Db        898 GGTGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTTTTGTATTGCGGAAAAAACGCG 957

Qy        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGCCACTA 1019

Db        958 CGCGAGGCAGCATTAACGTTATTAGGTCGCGCCCGCAAGGAAGAGCTGAGTCGCCACTA 1016


RESULT 10
ACA54019
ID   ACA54019 standard; DNA; 1020 BP.
XX
AC   ACA54019;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #35676.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Yersinia pestis.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU50149.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 41889; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1020 BP; 238 A; 238 C; 288 G; 256 T; 0 U; 0 Other;

  Query Match           59.4%;  Score 606;  DB 8;  Length 1020;
  Best Local Similarity   74.9%;  Pred. No. 9.5e-179;
  Matches  759;  Conservative    0;  Mismatches  255;  Indels    0;  Gaps    0;
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```
Qy          1 ATGAACCAACGTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTT 60
              ||||||         |||||||||| |||| |||||||||| || ||||||||||  |
Db          1 ATGAACACCAACCCTGCTTCAATGGCTGTTATCGGTGCCGGATCTTACGGCACCGCATTA 60

Qy         61 GCCATCACCCTGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACAT 120
              || ||||| |||||  | ||||||||  | ||  ||  | ||||||||||||||| |||||
Db         61 GCTATCACACTGGCGCGTAATGGCCATCAAGTCGTGTTATGGGGCCATGACCCTAAACAT 120

Qy        121 ATCGCAACGCTTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCC 180
              ||   |  |||  |||  ||||||||||||  ||| || || || ||||   |||| |||
Db        121 ATTCAACAGCTGCAACAAGACCGCTGTAACCGCGCTTTCCTACCTGATGCTGCTTTCCCC 180

Qy        181 GATACGCTCCATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTC 240
              ||||||  |  |  |||| |||  | ||   |||| |||| ||||||||  ||  |  |
Db        181 GATACGTTGCGATTGGAAACCGACTTAGCATGTGCGTTGGCTGCCAGCCGCGATGTGTTG 240

Qy        241 GTCGTCGTACCCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGT 300
              |||||||| ||||||||||||||||||  ||  | |  ||| | || || |   | |||
Db        241 GTCGTCGTGCCCAGCCATGTCTTTGGTGCTGTTTTACATCAGTTGAAGCCTCATCTACGT 300

Qy        301 CCTGATGCGCGTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTA 360
              |||||  |||  |  ||  |||||  |||||||||||  |||||  ||||||||  ||||||  ||
Db        301 AAAGATGCACGTATCGTCTGGGCAACCAAAGGGCTAGAAGCTGAAACCGGCCGTCTGCTA 360

Qy        361 CAGGACGTGGCGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCA 420
              |||||  |||||  ||  ||  |  |||  |||||     ||  |||||  ||  ||  ||||||  |||
Db        361 CAGGATGTGGCCCGCGAAGTCTTGGGCGAGGCTATCCCGCTTGCCGTGATTTCTGGTCCA 420

Qy        421 ACGTTTGCGAAAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGAT 480
              |||||||  ||||||  ||||  ||  |||||  ||  ||  ||  |||  ||  ||||  |||||||||
Db        421 ACGTTTGCCAAAGAATTGGCCGCGGGTTTGCCTACGGCGATTGCGTTGGCATCGACCGAT 480

Qy        481 CAGACCTTTGCCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTAC 540
                  |   |||  |||  |||||  ||  |||  |   |||||||  ||  |||||  ||  ||  ||||||
Db        481 GTGCAATTTAGCGAAGATCTGCAACAGTTATTGCACTGTGGAAAAAGCTTTCGAGTTTAC 540

Qy        541 AGCAATCCGGATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATT 600
              ||  |||||  |||||  ||  ||  ||  ||||||||  |||||  ||||||||||  ||||||||
Db        541 AGTAATCCTGATTTTATCGGGGTACAGCTTGGTGGCGCAGTGAAAAACGTGATTGCCATC 600

Qy        601 GGTGCGGGGATGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACC 660
              |||||  ||  ||||||||  ||  ||||||||||||||||||||  |||||  ||  ||  |||
Db        601 GGTGCAGGTATGTCCGATGGCATCGGTTTTGGTGCGAATGCCCGTACCGCTCTAATAACC 660

Qy        661 CGTGGGCTGGCTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTT 720
              ||  |||  |  ||  ||  |||  ||||  |  ||  ||||  |  ||||||||  |||  ||||||||
Db        661 CGCGGGTTAGCGGAGATGACGCGCTTAGGGACGGCATTAGGTGCCGATCCTTCCACCTTT 720

Qy        721 ATGGGCATGGCGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAAC 780
              ||||||||||  |||  |  ||||||  |||||||  |||||  ||  ||  |||||  ||  ||||||
Db        721 ATGGGCATGGCAGGGTTAGGCGATTTGGTGCTAACCTGCACAGATAACCAATCCCGTAAC 780

Qy        781 CGCCGTTTTGGCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATT 840
              |||||  ||||||||  |||||  ||||||||  |||  ||  |  |||||||  ||  |||
Db        781 CGCCGATTTGGCATTATGCTGGGTCAGGGGTTGGGGGTGAAGGAGGCGCAGGACAACATT 840

Qy        841 GGTCAGGTGGTGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTC 900
              |||||  |||||  |||||  |||||  |||||  ||  |||||  |  |  |  |  ||  ||  ||
Db        841 GGTCAAGTGGTAGAAGGTTACCGTAATACCAAGGAAGTTCTGGCATTAGCACAGCGTCAT 900

Qy        901 GGCGTTGAAATGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCG 960
              |||||  ||||||||||||||  ||  ||||||||||||  ||  |||||     ||  ||  ||
Db        901 GGCGTCGAAATGCCAATAACTGAACAAATTTATCAAGTGTTGTATTGTCATAAGAATGCT 960

Qy        961 CGCGAGGCAGCATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGCAGCAGC 1014
              ||  |||||  ||  ||||  ||  ||  ||  |     ||  ||  ||     |  |  ||
Db        961 CGTGAGGCGGCTCTGACGTTGTTGGGGCGGACCAAAAAAGATGAAAAAATCGGC 1014


RESULT 11
ABQ21987/c
ID   ABQ21987 standard; DNA; 781 BP.
XX
AC   ABQ21987;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 8578.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful for
PT   diagnosis and prognosis, comprises selective hybridization of amplicons
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one member,
CC   of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC   degree of hybridisation to both classes is determined from the label on
CC   the amplicon. From the ratio of labels hybridised to the two classes of
CC   oligomers, the degree of methylation is calculated. The method is used:
CC   (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC   and of a wide range of diseases, e.g. cancer, disorders of the central
CC   nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC   particularly by detecting mutations or single nucleotide polymorphisms
CC   (SNP's); and (ii) for differentiation of cell or tissue types and for
CC   investigating cell differentiation. The method allows the methylation
CC   status of many C residues to be determined simultaneously. ABQ13410-
CC   ABQ54121 represent genomic DNA sequences used to illustrate the method
CC   for determining the degree of cytosine methylation described in the
CC   disclosure of the invention
XX
SQ   Sequence 781 BP; 313 A; 239 C; 76 G; 153 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 565.6;  DB 6;  Length 781;
  Best Local Similarity   82.8%;  Pred. No. 3.7e-166;
  Matches  646;  Conservative    0;  Mismatches  134;  Indels    0;  Gaps    0;

Qy        153 CGCGTTTCTCCCCGATGTGCCTTTTCCCGATACGCTCCATCTTGAAAGCGATCTCGCCAC 212
              |||||||  |   |||||||  |||   |||||||  |  || |||||||  ||  |||  |
Db        780 CGCGTTTTTTTTCGATGTGTTTTTATTCGATACGTTTTATTTTGAAAGTAATTTCGTTAT 721

Qy        213 TGCGCTGGCAGCCAGCCGTAATATTCTCGTCGTCGTACCCAGCCATGTCTTTGGTGAAGT 272
              ||||  |||  ||  ||  ||||||||||  ||||||||||    ||  ||||  ||||||||||
Db        720 TGCGTTGGTAGTTAGTCGTAATATTTTCGTCGTCGTATTTAGTTATGTTTTTGGTGAAGT 661

Qy        273 GCTGCGCCAGATTAAACCACTGATGCGTCCTGATGCGCGTCTGGTGTGGGCGACCAAAGG 332
              |  ||||  ||||||||  |  ||||||||  ||||||||||  ||||||||||||  |||||
Db        660 GTTGCGTTAGATTAAATTATTGATGCGTTTTGATGCGCGTTTGGTGTGGGCGATTAAAGG 601
```

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Qy        333 GCTGGAAGCGGAAACCGGACGTCTGTTACAGGACGTGGCGCGTGAGGCCTTAGGCGATCA 392
              | |||||||||||| ||||||| ||||| |||||||||||||||| |  |||||||| |
Db        600 GTTGGAAGCGGAAATCGGACGTTTGTTATAGGACGTGGCGCGTGATGTTTTAGGCGATTA 541

Qy        393 AATTCCGCTGGCGGTTATCTCTGGCCCAACGTTTGCGAAAGAACTGGCGGCAGGTTTACC 452
              |||| || |||||||||| | |||   |||||||||||||||| |||||| |||||||  |
Db        540 AATTTCGTTGGCGGTTATTTTTGGTTTAACGTTTGCGAAAGAATTGGCGGTAGGTTTATC 481

Qy        453 GACAGCTATTTCGCTGGCCTCGACCGATCAGACCTTTGCCGATGATCTCCAGCAGCTGCT 512
              || || ||||||| |||  |||| |||| |||  |||| |||||||  |  || || || |
Db        480 GATAGTTATTTCGTTGGTTTCGATCGATTAGATTTTTGTCGATGATTTTTAGTAGTTGTT 421

Qy        513 GCACTGCGGCAAAAGTTTCCGCGTTTACAGCAATCCGGATTTCATTGGCGTGCAGCTTGG 572
              | | ||||| |||||||| |||||||| || ||| ||||||| |||||||| || ||||
Db        420 GTATTGCGGTAAAAGTTTTCGCGTTTATAGTAATTCGGATTTTATTGGCGTGTAGTTTGG 361

Qy        573 CGGCGCGGTGAAAAACGTTATTGCCATTGGTGCGGGGATGTCCGACGGTATCGGTTTTGG 632
              |||||||||||||||||||||  |||||||||||||||| ||||||||||||||||||||
Db        360 CGGCGCGGTGAAAAACGTTATTGTTATTGGTGCGGGGATGTTCGACGGTATCGGTTTTGG 301

Qy        633 TGCGAATGCGCGTACGGCGCTGATCACCCGTGGGCTGGCTGAAATGTCGCGTCTTGGTGC 692
              |||||||||||||||||| |||| |  |||||| ||| |||||||||||| |||||||
Db        300 TGCGAATGCGCGTACGGCGTTGATTATTCGTGGGTTGGTTGAAATGTCGCGTTTTGGTGC 241

Qy        693 GGCGCTGGGTGCCGACCCTGCCACCTTTATGGGCATGGCGGGGCTTGGCGATCTGGTGCT 752
              |||| |||||| |||   ||  |  |||||||| |||||||| |||||||| ||||| |
Db        240 GGCGTTGGGTGTCGATTTTGTTATTTTTATGGGTATGGCGGGGTTTGGCGATTTGGTGTT 181

Qy        753 TACCTGTACCGAAAACCAGTCGCGTAACCGCCGTTTTGGCATGATGCTCGGTCAGGGCAT 812
              ||  |||| ||| ||  |||||||||| || |||||||| |||||| ||||| |||| ||
Db        180 TATTTGTATCGATAATTAGTCGCGTAATCGTCGTTTTGGTATGATGTTCGGTTAGGGTAT 121

Qy        813 GGATGTACAAAGCGCGCAGGAGAAGATTGGTCAGGTGGTGGAAGGCTACCGCAATACGAA 872
              ||||||| |||||||| |||||||||||||| |||||||||||| || || ||||||||
Db        120 GGATGTATAAAGCGCGTAGGAGAAGATTGGTTAGGTGGTGGAAGGTTATCGTAATACGAA 61

Qy        873 AGAAGTCCGCGAACTGGCGCATCGCTTCGGCGTTGAAATGCCAATAACCGAGGAAATTTA 932
              |||||| |||||| ||||| |||| ||||||||||||||  ||||| ||||||||||||
Db         60 AGAAGTTCGCGAATTGGCGTATCGTTTCGGCGTTGAAATGTTAATAATCGAGGAAATTTA 1
```

RESULT 12
ABQ21986
ID ABQ21986 standard; DNA; 781 BP.
XX
AC ABQ21986;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 8577.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 781 BP; 153 A; 76 C; 239 G; 313 T; 0 U; 0 Other;

Query Match 55.5%; Score 565.6; DB 6; Length 781;
Best Local Similarity 82.8%; Pred. No. 3.7e-166;
Matches 646; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

```
Qy        153 CGCGTTTCTCCCCGATGTGCCTTTTCCCGATACGCTCCATCTTGAAAGCGATCTCGCCAC 212
              |||||||  |   |||||||  |||   |||||||  |  || |||||||  || |||  |
Db          2 CGCGTTTTTTTTCGATGTGTTTTTATTCGATACGTTTTATTTTGAAAGTAATTTCGTTAT 61

Qy        213 TGCGCTGGCAGCCAGCCGTAATATTCTCGTCGTCGTACCCAGCCATGTCTTTGGTGAAGT 272
              |||| ||| ||  ||  |||||||| ||||||||||   ||  |||| ||||||||||
Db         62 TGCGTTGGTAGTTAGTCGTAATATTTTCGTCGTCGTATTTAGTTATGTTTTTGGTGAAGT 121

Qy        273 GCTGCGCCAGATTAAACCACTGATGCGTCCTGATGCGCGTCTGGTGTGGGCGACCAAAGG 332
              | ||||  ||||||||  | ||||||||  |||||||||| |||||||||||  |||||
Db        122 GTTGCGTTAGATTAAATTATTGATGCGTTTTGATGCGCGTTTGGTGTGGGCGATTAAAGG 181

Qy        333 GCTGGAAGCGGAAACCGGACGTCTGTTACAGGACGTGGCGCGTGAGGCCTTAGGCGATCA 392
              | |||||||||||| ||||||| ||||| |||||||||||||||| |  |||||||| |
Db        182 GTTGGAAGCGGAAATCGGACGTTTGTTATAGGACGTGGCGCGTGATGTTTTAGGCGATTA 241

Qy        393 AATTCCGCTGGCGGTTATCTCTGGCCCAACGTTTGCGAAAGAACTGGCGGCAGGTTTACC 452
              |||| || |||||||||| | |||   |||||||||||||||| |||||| |||||||  |
Db        242 AATTTCGTTGGCGGTTATTTTTGGTTTAACGTTTGCGAAAGAATTGGCGGTAGGTTTATC 301

Qy        453 GACAGCTATTTCGCTGGCCTCGACCGATCAGACCTTTGCCGATGATCTCCAGCAGCTGCT 512
              || || ||||||| |||  |||| |||| |||  |||| |||||||  |  || || || |
Db        302 GATAGTTATTTCGTTGGTTTCGATCGATTAGATTTTTGTCGATGATTTTTAGTAGTTGTT 361

Qy        513 GCACTGCGGCAAAAGTTTCCGCGTTTACAGCAATCCGGATTTCATTGGCGTGCAGCTTGG 572
              | | ||||| |||||||| |||||||| || ||| ||||||| |||||||| || ||||
Db        362 GTATTGCGGTAAAAGTTTTCGCGTTTATAGTAATTCGGATTTTATTGGCGTGTAGTTTGG 421

Qy        573 CGGCGCGGTGAAAAACGTTATTGCCATTGGTGCGGGGATGTCCGACGGTATCGGTTTTGG 632
              |||||||||||||||||||||  |||||||||||||||| ||||||||||||||||||||
Db        422 CGGCGCGGTGAAAAACGTTATTGTTATTGGTGCGGGGATGTTCGACGGTATCGGTTTTGG 481

Qy        633 TGCGAATGCGCGTACGGCGCTGATCACCCGTGGGCTGGCTGAAATGTCGCGTCTTGGTGC 692
              |||||||||||||||||| |||| |  |||||| ||| |||||||||||| |||||||
Db        482 TGCGAATGCGCGTACGGCGTTGATTATTCGTGGGTTGGTTGAAATGTCGCGTTTTGGTGC 541

Qy        693 GGCGCTGGGTGCCGACCCTGCCACCTTTATGGGCATGGCGGGGCTTGGCGATCTGGTGCT 752
              |||| |||||| |||   ||  |  |||||||| |||||||| |||||||| ||||| |
Db        542 GGCGTTGGGTGTCGATTTTGTTATTTTTATGGGTATGGCGGGGTTTGGCGATTTGGTGTT 601
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Qy        753 TACCTGTACCGAAAACCAGTCGCGTAACCGCCGTTTTGGCATGATGCTCGGTCAGGGCAT 812
              ||  |||| ||| ||  |||||||||| || |||||||| |||||| ||||| |||| ||
Db        602 TATTTGTATCGATAATTAGTCGCGTAATCGTCGTTTTGGTATGATGTTCGGTTAGGGTAT 661

Qy        813 GGATGTACAAAGCGCGCAGGAGAAGATTGGTCAGGTGGTGGAAGGCTACCGCAATACGAA 872
              ||||||| |||||||| |||||||||||||| |||||||||||||| || || ||||||||
Db        662 GGATGTATAAAGCGCGTAGGAGAAGATTGGTTAGGTGGTGGAAGGTTATCGTAATACGAA 721

Qy        873 AGAAGTCCGCGAACTGGCGCATCGCTTCGGCGTTGAAATGCCAATAACCGAGGAAATTTA 932
              |||||| |||||| ||||| |||| ||||||||||||||  ||||| ||||||||||||
Db        722 AGAAGTTCGCGAATTGGCGTATCGTTTCGGCGTTGAAATGTTAATAATCGAGGAAATTTA 781
```

RESULT 13
ACF70491
ID ACF70491 standard; DNA; 1023 BP.
XX
AC ACF70491;
XX
DT 20-NOV-2003 (first entry)
XX
DE Photorhabdus luminescens nucleotide sequence #8958.
XX
KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough; gene; ds.
XX
OS Photorhabdus luminescens.
XX
PN WO200294867-A2.
XX
PD 28-NOV-2002.
XX
PF 07-FEB-2002; 2002WO-IB003040.
XX
PR 07-FEB-2001; 2001FR-00001659.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
DR WPI; 2003-148459/14.
XX
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 2; SEQ ID NO 8958; 1205pp; French.
XX
CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens genes

XX
SQ Sequence 1023 BP; 260 A; 197 C; 275 G; 291 T; 0 U; 0 Other;

Query Match 54.5%; Score 556.4; DB 10; Length 1023;
Best Local Similarity 72.3%; Pred. No. 3.2e-163;
Matches 722; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

```
Qy         11 GTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTTGCCATCACCC 70
              ||| || ||| ||||| ||||| |||||||||| |||||||| |  | ||||| || |
Db          8 GTACTGTTTCTATGACAGTGATTGGTGCCGGCTCATACGGCACCTCATTAGCCATTACGC 67

Qy         71 TGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACATATCGCAACGC 130
              ||||  | ||||| ||  | ||||| || ||||| ||| | || || ||| | |   |
Db         68 TGGCTCGTAATGGTCATAATGTTGTACTTTGGGGGCATAATCCAGAGCATGTTGGGGCAT 127

Qy        131 TTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCCGATACGCTCC 190
              |  |||| |  || |||||       ||||| || |||||  | |||||  ||||   |
Db        128 TGCAACGGGTGCGTTGTAATCAAAAATTTCTGCCGGATGTTTCCTTTCCTGATAGTTTAT 187

Qy        191 ATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTCGTCGTCGTAC 250
              |||||||  || ||    |  || ||  |||| |||||  |||||||  || || ||||
Db        188 TGCTTGAAACGGACCTAATAAAAGCACTAACAGCGAGCCGCGATATTCTTGTTGTGGTAC 247

Qy        251 CCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGTCCTGATGCGC 310
              | |||||||| |||||||||||| |    ||||| |||||||   | || |||||| | |
Db        248 CTAGCCATGTGTTTGGTGAAGTGTTAAAGCAGATAAAACCACATTTACGGCCTGATTCAC 307

Qy        311 GTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTACAGGACGTGG 370
              || | || ||||| || |||||  |||||||||| ||||| ||  | || ||||| ||||
Db        308 GTATCGTATGGGCAACTAAAGGCTTGGAAGCGGATACCGGTCGGTTATTGCAGGATGTGG 367

Qy        371 CGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCAACGTTTGCGA 430
              | ||||||  |||||| || |||| ||||| |||||  ||||||| ||||| ||||| |
Db        368 CCCGTGAGATATTAGGCAATGAAATACCGCTAGCGGTGCTCTCTGGGCCAACATTTGCTA 427

Qy        431 AAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGATCAGACCTTTG 490
              ||||  | ||||| ||||| || || || ||| |  |  || |||| ||     | ||||
Db        428 AAGAGTTAGCGGCTGGTTTGCCTACCGCGATTGCTATTTCCGCGACGGAATCTGCTTTTG 487

Qy        491 CCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTACAGCAATCCGG 550
               |||||  || || ||  |  | ||||| |||||||||||||| ||||| |  ||||| |
Db        488 GCGATGGACTTCAACAATTATTCCACTGTGGCAAAAGTTTCCGGGTTTATAAAAATCCTG 547

Qy        551 ATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATTGGTGCGGGGA 610
              |||| ||||| || || || || || || || |||||||| || |||||||| ||||| |
Db        548 ATTTTATTGGTGTTCAACTCGGTGGTGCCGTAAAAAACGTGATCGCCATTGGCGCGGGAA 607

Qy        611 TGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACCCGTGGGCTGG 670
              | || || || || || |||||||| ||||| ||||| ||  |||| || |||||  |||
Db        608 TATCTGATGGCATGGGATTTGGTGCTAATGCTCGTACCGCATTGATTACTCGTGGATTGG 667

Qy        671 CTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTTATGGGCATGG 730
              | ||||||   || |||||||| ||||| ||||| || ||| | ||||||||||||||||
Db        668 CGGAAATGAGTCGCCTTGGTGCAGCGCTTGGTGCTGATCCTTCTACCTTTATGGGCATGG 727

Qy        731 CGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAACCGCCGTTTTG 790
              ||||  | |||||| ||||  | || ||||| || ||||| || |||||||| |||||||
Db        728 CGGGATTGGGCGATTTGGTCTTAACTTGTACTGATAACCAATCACGTAACCGTCGTTTTG 787

Qy        791 GCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATTGGTCAGGTGG 850
              |||||||||| || ||||| ||   |||  ||   |||||| |  ||||||| ||||| |
Db        788 GCATGATGCTGGGGCAGGGAATCAGTGTTGAAGAAGCGCAGTATCAGATTGGGCAGGTTG 847

Qy        851 TGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTCGGCGTTGAAA 910
              | ||||| || |||||||| |||||||| || | | ||||  |||||  |   || ||||
Db        848 TTGAAGGTTATCGCAATACCAAAGAAGTACGTGCATTGGCTAATCGCGCCAATGTAGAAA 907

Qy        911 TGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCGCGCGAGGCAG 970
              |||| ||  | ||  |||| || ||  || | |||||||   ||||| | |   || || |
Db        908 TGCCGATTGCAGAACAAATCTACCAGATACTCTATTGCAATAAAAATGTGATAGAAGCTG 967

Qy        971 CATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGC 1008
              |   | | ||| ||||  | ||  | ||||| ||| ||
```

```
Db        968 CTCAGGCATTATTAGGAAGAGCCAGAAAGGATGAGAGC 1005


RESULT 14
ACF65374
ID   ACF65374 standard; DNA; 69727 BP.
XX
AC   ACF65374;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Photorhabdus luminescens nucleotide sequence #27.
XX
KW   Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW   detection; food; gene expression; plant; animal; microorganism; toxin;
KW   antibiotic; biopesticide; virulence factor; disease model; plague;
KW   whooping cough; gene; ds.
XX
OS   Photorhabdus luminescens.
XX
PN   WO200294867-A2.
XX
PD   28-NOV-2002.
XX
PF   07-FEB-2002; 2002WO-IB003040.
XX
PR   07-FEB-2001; 2001FR-00001659.
XX
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Duchaud E,  Taourit S,  Glaser P,  Frangeul L,  Kunst F,  Danchin A;
PI   Buchrieser C;
XX
DR   WPI; 2003-148459/14.
XX
PT   Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT   useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS   Claim 1; SEQ ID NO 27; 1205pp; French.
XX
CC   The invention relates to the isolation of genes and their encoded
CC   proteins from Photorhabdus luminescens. The isolated sequences are
CC   sources of probes and primers for detecting the genome of P. luminescens
CC   and related species; to study polymorphisms; for gene analysis and for
CC   detection/amplification of the genes. Antibodies (Ab) raised against the
CC   polypeptides encoded by the genes are used for detection/identification
CC   of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC   carry a gene-containing vector are used to select compounds that
CC   modulate, regulate, induce or inhibit expression of the genes in plants,
CC   animals or microorganisms other than P. luminescens and are able to alter
CC   response or sensitivity to toxins and antibiotics produced by P.
CC   luminescens. Cells transformed to express the genes are useful for
CC   recombinant production of the proteins, particularly toxins and
CC   antibacterials useful as insecticides, bactericides and fungicides. The
CC   genes, proteins, vectors containing the genes and Ab are also useful
CC   therapeutically (to treat microbial infection by bacteria or fungi that
CC   are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC   biopesticides. Other uses of the genes and the proteins are as virulence
CC   factors and for identifying targets of human diseases for which P.
CC   luminescens is a model (particularly plague and whooping cough). This
CC   sequence represents one of the isolated P. luminescens genes
XX
SQ   Sequence 69727 BP; 20213 A; 13239 C; 14632 G; 21638 T; 0 U; 5 Other;

  Query Match             54.5%;  Score 556.4;  DB 10;  Length 69727;
  Best Local Similarity   72.3%;  Pred. No. 2.5e-162;
  Matches  722;  Conservative    0;  Mismatches  276;  Indels    0;  Gaps    0;

Qy          11 GTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTTGCCATCACCC 70
               ||| || ||| ||||| ||||| |||||||||||| ||||||||| |   | ||||| || |
Db       54182 GTACTGTTTCTATGACAGTGATTGGTGCCGGCTCATACGGCACCTCATTAGCCATTACGC 54241

Qy          71 TGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACATATCGCAACGC 130
               |||| | ||||| ||  | ||||| || ||||| ||| | || || ||| | |   |
Db       54242 TGGCTCGTAATGGTCATAATGTTGTACTTTGGGGGCATAATCCAGAGCATGTTGGGGCAT 54301

Qy         131 TTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCCGATACGCTCC 190
               | |||| |  || |||||       ||||| || ||||| | ||||| |||| |
Db       54302 TGCAACGGGTGCGTTGTAATCAAAAATTTCTGCCGGATGTTTCCTTTCCTGATAGTTTAT 54361

Qy         191 ATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTCGTCGTCGTAC 250
                |||||||  || ||    | || ||  |||| |||||  ||||||| || || ||||
Db       54362 TGCTTGAAACGGACCTAATAAAAGCACTAACAGCGAGCCGCGATATTCTTGTTGTGGTAC 54421

Qy         251 CCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGTCCTGATGCGC 310
               | |||||||| |||||||||||| |     ||||| |||||||    | || |||||| | |
Db       54422 CTAGCCATGTGTTTGGTGAAGTGTTAAAGCAGATAAAACCACATTTACGGCCTGATTCAC 54481

Qy         311 GTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTACAGGACGTGG 370
               || | || ||||| || ||||| |||||||||| ||||| ||  | || ||||| ||||
Db       54482 GTATCGTATGGGCAACTAAAGGCTTGGAAGCGGATACCGGTCGGTTATTGCAGGATGTGG 54541

Qy         371 CGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCAACGTTTGCGA 430
               | ||||||    |||||| || |||| |||| ||||  ||||||| ||||| ||||| |
Db       54542 CCCGTGAGATATTAGGCAATGAAATACCGCTAGCGGTGCTCTCTGGGCCAACATTTGCTA 54601

Qy         431 AAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGATCAGACCTTTG 490
               |||| | ||||| ||||| || || || ||| |  |  || |||| ||      | ||||
Db       54602 AAGAGTTAGCGGCTGGTTTGCCTACCGCGATTGCTATTTCCGCGACGGAATCTGCTTTTG 54661

Qy         491 CCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTACAGCAATCCGG 550
               |||||  || || ||  |  | ||||| |||||||||||||| |||||  |  ||||| |
Db       54662 GCGATGGACTTCAACAATTATTCCACTGTGGCAAAAGTTTCCGGGTTTATAAAAATCCTG 54721

Qy         551 ATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATTGGTGCGGGGA 610
               |||| ||||| || || || || || || || |||||||| || |||||||| ||||| |
Db       54722 ATTTTATTGGTGTTCAACTCGGTGGTGCCGTAAAAAACGTGATCGCCATTGGCGCGGGAA 54781

Qy         611 TGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACCCGTGGGCTGG 670
               | || || || || || |||||||| ||||| ||||| ||  |||| || |||  |||
Db       54782 TATCTGATGGCATGGGATTTGGTGCTAATGCTCGTACCGCATTGATTACTCGTGGATTGG 54841

Qy         671 CTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTTATGGGCATGG 730
               | ||||||    || |||||||| ||||| ||||| || ||| | ||||||||||||||||
Db       54842 CGGAAATGAGTCGCCTTGGTGCAGCGCTTGGTGCTGATCCTTCTACCTTTATGGGCATGG 54901

Qy         731 CGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAACCGCCGTTTTG 790
               ||||  | |||||| ||||  | || ||||| || ||||| || |||||||| |||||||
Db       54902 CGGGATTGGGCGATTTGGTCTTAACTTGTACTGATAACCAATCACGTAACCGTCGTTTTG 54961

Qy         791 GCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATTGGTCAGGTGG 850
               |||||||||| || ||||| ||   |||  ||   |||||| |  ||||||| ||||| |
Db       54962 GCATGATGCTGGGGCAGGGAATCAGTGTTGAAGAAGCGCAGTATCAGATTGGGCAGGTTG 55021

Qy         851 TGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTCGGCGTTGAAA 910
               | ||||| || |||||||| |||||||| || | | |||| |||||  |   || ||||
Db       55022 TTGAAGGTTATCGCAATACCAAAGAAGTACGTGCATTGGCTAATCGCGCCAATGTAGAAA 55081

Qy         911 TGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCGCGCGAGGCAG 970
               |||| ||  | ||  |||| || ||  || | ||||||   |||||  |  |   || || |
Db       55082 TGCCGATTGCAGAACAAATCTACCAGATACTCTATTGCAATAAAAATGTGATAGAAGCTG 55141

Qy         971 CATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGC 1008
               |   | | ||| ||||  | ||  | ||||| ||| ||
Db       55142 CTCAGGCATTATTAGGAAGAGCCAGAAAGGATGAGAGC 55179


RESULT 15
ACF67367_35
Continuation (36 of 57) of ACF67367 from base 3500001 (Photorhabdus luminescens nucleoti
WP Sequence split into 57 fragments  LOCUS ACF67367 Accession Acf67367
WP      Fragment Name       Begin      End
WP      ACF67367_00             1    110000
WP      ACF67367_01        100001    210000
WP      ACF67367_02        200001    310000
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WP	ACF67367_03	300001	410000
WP	ACF67367_04	400001	510000
WP	ACF67367_05	500001	610000
WP	ACF67367_06	600001	710000
WP	ACF67367_07	700001	810000
WP	ACF67367_08	800001	910000
WP	ACF67367_09	900001	1010000
WP	ACF67367_10	1000001	1110000
WP	ACF67367_11	1100001	1210000
WP	ACF67367_12	1200001	1310000
WP	ACF67367_13	1300001	1410000
WP	ACF67367_14	1400001	1510000
WP	ACF67367_15	1500001	1610000
WP	ACF67367_16	1600001	1710000
WP	ACF67367_17	1700001	1810000
WP	ACF67367_18	1800001	1910000
WP	ACF67367_19	1900001	2010000
WP	ACF67367_20	2000001	2110000
WP	ACF67367_21	2100001	2210000
WP	ACF67367_22	2200001	2310000
WP	ACF67367_23	2300001	2410000
WP	ACF67367_24	2400001	2510000
WP	ACF67367_25	2500001	2610000
WP	ACF67367_26	2600001	2710000
WP	ACF67367_27	2700001	2810000
WP	ACF67367_28	2800001	2910000
WP	ACF67367_29	2900001	3010000
WP	ACF67367_30	3000001	3110000
WP	ACF67367_31	3100001	3210000
WP	ACF67367_32	3200001	3310000
WP	ACF67367_33	3300001	3410000
WP	ACF67367_34	3400001	3510000
WP	ACF67367_35	3500001	3610000
WP	ACF67367_36	3600001	3710000
WP	ACF67367_37	3700001	3810000
WP	ACF67367_38	3800001	3910000
WP	ACF67367_39	3900001	4010000
WP	ACF67367_40	4000001	4110000
WP	ACF67367_41	4100001	4210000
WP	ACF67367_42	4200001	4310000
WP	ACF67367_43	4300001	4410000
WP	ACF67367_44	4400001	4510000
WP	ACF67367_45	4500001	4610000
WP	ACF67367_46	4600001	4710000
WP	ACF67367_47	4700001	4810000
WP	ACF67367_48	4800001	4910000
WP	ACF67367_49	4900001	5010000
WP	ACF67367_50	5000001	5110000
WP	ACF67367_51	5100001	5210000
WP	ACF67367_52	5200001	5310000
WP	ACF67367_53	5300001	5410000
WP	ACF67367_54	5400001	5510000
WP	ACF67367_55	5500001	5610000
WP	ACF67367_56	5600001	5648894

Query Match 54.5%; Score 556.4; DB 10; Length 110000;
Best Local Similarity 72.3%; Pred. No. 3.1e-162;
Matches 722; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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Qy        11 GTAATGCTTCAATGACTGTGATCGGTGCCGGCTCGTACGGCACCGCTCTTGCCATCACCC 70
             ||| || ||| ||||| ||||| |||||||||| ||||||||| |  | ||||| || |
Db     79833 GTACTGTTTCTATGACAGTGATTGGTGCCGGCTCATACGGCACCTCATTAGCCATTACGC 79892

Qy        71 TGGCAAGAAATGGCCACGAGGTTGTCCTCTGGGGCCATGACCCTGAACATATCGCAACGC 130
             ||||  | ||||| ||  | ||||| || ||||| ||| | || || ||| | |   |
Db     79893 TGGCTCGTAATGGTCATAATGTTGTACTTTGGGGGCATAATCCAGAGCATGTTGGGGCAT 79952

Qy       131 TTGAACGCGACCGCTGTAACGCCGCGTTTCTCCCCGATGTGCCTTTTCCCGATACGCTCC 190
             |  |||| |  || |||||       ||||| || |||||  | ||||| ||||   |
Db     79953 TGCAACGGGTGCGTTGTAATCAAAAATTTCTGCCGGATGTTTCCTTTCCTGATAGTTTAT 80012

Qy       191 ATCTTGAAAGCGATCTCGCCACTGCGCTGGCAGCCAGCCGTAATATTCTCGTCGTCGTAC 250
               |||||||  || ||    |  || ||  |||| |||||  ||||||| || || ||||
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Db     80013 TGCTTGAAACGGACCTAATAAAAGCACTAACAGCGAGCCGCGATATTCTTGTTGTGGTAC 80072

Qy       251 CCAGCCATGTCTTTGGTGAAGTGCTGCGCCAGATTAAACCACTGATGCGTCCTGATGCGC 310
             | |||||||| |||||||||||| |    ||||| |||||||   | || |||||| | |
Db     80073 CTAGCCATGTGTTTGGTGAAGTGTTAAAGCAGATAAAACCACATTTACGGCCTGATTCAC 80132

Qy       311 GTCTGGTGTGGGCGACCAAAGGGCTGGAAGCGGAAACCGGACGTCTGTTACAGGACGTGG 370
             || | || ||||| || |||||  |||||||||| ||||| ||  | || ||||| ||||
Db     80133 GTATCGTATGGGCAACTAAAGGCTTGGAAGCGGATACCGGTCGGTTATTGCAGGATGTGG 80192

Qy       371 CGCGTGAGGCCTTAGGCGATCAAATTCCGCTGGCGGTTATCTCTGGCCCAACGTTTGCGA 430
             | ||||||   ||||||  || |||| ||||| |||||  ||||||| ||||| ||||| |
Db     80193 CCCGTGAGATATTAGGCAATGAAATACCGCTAGCGGTGCTCTCTGGGCCAACATTTGCTA 80252

Qy       431 AAGAACTGGCGGCAGGTTTACCGACAGCTATTTCGCTGGCCTCGACCGATCAGACCTTTG 490
             ||||  | ||||| ||||| || || || ||| |  |  || |||| ||      | ||||
Db     80253 AAGAGTTAGCGGCTGGTTTGCCTACCGCGATTGCTATTTCCGCGACGGAATCTGCTTTTG 80312

Qy       491 CCGATGATCTCCAGCAGCTGCTGCACTGCGGCAAAAGTTTCCGCGTTTACAGCAATCCGG 550
              |||||  || || ||  |  | ||||| |||||||||||||| ||||| |  |||||  |
Db     80313 GCGATGGACTTCAACAATTATTCCACTGTGGCAAAAGTTTCCGGGTTTATAAAAATCCTG 80372

Qy       551 ATTTCATTGGCGTGCAGCTTGGCGGCGCGGTGAAAAACGTTATTGCCATTGGTGCGGGGA 610
             |||| ||||| || || || || || || || |||||||| || |||||||| ||||| |
Db     80373 ATTTTATTGGTGTTCAACTCGGTGGTGCCGTAAAAAACGTGATCGCCATTGGCGCGGGAA 80432

Qy       611 TGTCCGACGGTATCGGTTTTGGTGCGAATGCGCGTACGGCGCTGATCACCCGTGGGCTGG 670
             | || || || || || |||||||| ||||| ||||| ||  |||| || |||||  |||
Db     80433 TATCTGATGGCATGGGATTTGGTGCTAATGCTCGTACCGCATTGATTACTCGTGGATTGG 80492

Qy       671 CTGAAATGTCGCGTCTTGGTGCGGCGCTGGGTGCCGACCCTGCCACCTTTATGGGCATGG 730
             | ||||||   || |||||||| ||||| ||||| || ||| | ||||||||||||||||
Db     80493 CGGAAATGAGTCGCCTTGGTGCAGCGCTTGGTGCTGATCCTTCTACCTTTATGGGCATGG 80552

Qy       731 CGGGGCTTGGCGATCTGGTGCTTACCTGTACCGAAAACCAGTCGCGTAACCGCCGTTTTG 790
             ||||  | |||||| ||||  | || ||||| || ||||| || |||||||| ||||||||
Db     80553 CGGGATTGGGCGATTTGGTCTTAACTTGTACTGATAACCAATCACGTAACCGTCGTTTTG 80612

Qy       791 GCATGATGCTCGGTCAGGGCATGGATGTACAAAGCGCGCAGGAGAAGATTGGTCAGGTGG 850
             |||||||||| || ||||| ||   |||  ||   |||||| |  ||||||| ||||| |
Db     80613 GCATGATGCTGGGGCAGGGAATCAGTGTTGAAGAAGCGCAGTATCAGATTGGGCAGGTTG 80672

Qy       851 TGGAAGGCTACCGCAATACGAAAGAAGTCCGCGAACTGGCGCATCGCTTCGGCGTTGAAA 910
             | ||||| || |||||||| |||||||| || | | ||||  |||||  |   || ||||
Db     80673 TTGAAGGTTATCGCAATACCAAAGAAGTACGTGCATTGGCTAATCGCGCCAATGTAGAAA 80732

Qy       911 TGCCAATAACCGAGGAAATTTATCAAGTATTATATTGCGGAAAAAACGCGCGCGAGGCAG 970
             |||| ||  | ||  |||| || ||  || | ||||||   |||||  |  |  || || |
Db     80733 TGCCGATTGCAGAACAAATCTACCAGATACTCTATTGCAATAAAAATGTGATAGAAGCTG 80792

Qy       971 CATTGACTTTACTAGGTCGTGCACGCAAGGACGAGCGC 1008
             |   | | ||| ||||  | ||  | ||||| ||| ||
Db     80793 CTCAGGCATTATTAGGAAGAGCCAGAAAGGATGAGAGC 80830
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Search completed: April 27, 2005, 11:29:20
Job time : 666 secs